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(54) Method for producing L-lysine

(57) A recombinant DNA autonomously replicable in cells of coryneform bacteria, comprising a DNA sequence coding for an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and a DNA sequence coding for a diaminopimelate decarboxylase; a coryneform bacterium harboring an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and comprising an enhanced DNA sequence coding for a diaminopimelate decarboxylase; and a method for producing L-lysine comprising the steps of cultivating the coryneform bacterium in an appropriate medium to allow L-lysine to be produced and accumulated in a culture of the bacterium, and collecting L-lysine from the culture.

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Description

BACKGROUND OF THE INVENTION

5 The present invention relates to a method for producing L-lysine by cultivating a microorganism obtained by modifying a coryneform bacterium used for fermentative production of amino acid or the like by means of a technique based on genetic engineering.

L-Lysine, which is used as a fodder additive, is usually produced by a fermentative method by using an L-lysine-producing mutant strain belonging to the coryneform bacteria. Various L-lysine-producing bacteria known at present
10 are those created by artificial mutation starting from wild type strains belonging to the coryneform bacteria.

As for the coryneform bacteria, there are disclosed a vector plasmid which is autonomously replicable in bacterial cells and has a drug resistance marker gene (see United States Patent No. 4,514,502), and a method for introducing a gene into bacterial cells (for example, Japanese Patent Application Laid-open No. 2-207791). There is also disclosed a possibility for breeding an L-threonine- or L-isoleucine-producing bacterium by using the techniques as described
15 above (see United States Patent Nos. 4,452,890 and 4,442,208). As for breeding of an L-lysine-producing bacterium, a technique is known, in which a gene participating in L-lysine biosynthesis is incorporated into a vector plasmid to amplify the gene in bacterial cells (for example, Japanese Patent Application Laid-open No. 56-160997).

Known genes for L-lysine biosynthesis include, for example, a dihydrodipicolinate reductase gene (Japanese Patent Application Laid-open No. 7-75578) and a diaminopimelate dehydrogenase gene (Ishino, S. et al., Nucleic Acids Res., 15, 3917 (1987)) in which a gene participating in L-lysine biosynthesis is cloned, as well as a phosphoenolpyruvate carboxylase gene (Japanese Patent Application Laid-open No. 60-87788), a dihydrodipicolinate synthase gene (Japanese Patent Publication No. 6-55149), and a diaminopimelate decarboxylase gene (Japanese Patent Application Laid-open No. 60-62994) in which amplification of a gene affects L-lysine productivity.

As for enzymes participating in L-lysine biosynthesis, a case is known for an enzyme which undergoes feedback
25 inhibition when used as a wild type. In this case, L-lysine productivity is improved by introducing an enzyme gene having such mutation that the feedback inhibition is desensitized. Those known as such a gene specifically include, for example, an aspartokinase gene (International Publication Pamphlet of WO 94/25605).

As described above, certain successful results have been obtained by means of amplification of genes for the L-lysine biosynthesis system, or introduction of mutant genes. For example, a coryneform bacterium, which harbors a
30 mutant aspartokinase gene with desensitized concerted inhibition by lysine and threonine, produces a considerable amount of L-lysine (about 25 g/L). However, this bacterium suffers decrease in growth speed as compared with a bacterium harboring no mutant aspartokinase gene. It is also reported that L-lysine productivity is improved by further introducing a dihydrodipicolinate synthase gene in addition to a mutant aspartokinase gene (Applied and Environmental Microbiology, 57(6), 1746-1752 (1991)). However, such a bacterium suffers further decrease in growth speed.

No case has been reported in which growth is intended to be improved by enhancing a gene for L-lysine biosynthesis as well. In the present circumstances, no case is known for the coryneform bacteria, in which anyone has succeeded in remarkable improvement in L-lysine yield without restraining growth, by combining a plurality of genes for L-lysine biosynthesis.

SUMMARY OF THE INVENTION

An object of the present invention is to improve the L-lysine yield without restraining the growth of a coryneform bacterium, by enhancing a plurality of genes for L-lysine biosynthesis in combination in the coryneform bacteria.

When an objective substance is produced fermentatively by using a microorganism, the production speed, as well
45 as the yield of the objective substance relative to an introduced material, is an extremely important factor. An objective substance may be produced remarkably inexpensively by increasing the production speed per a unit of fermentation equipment. Accordingly, it is industrially extremely important that the fermentative yield and the production speed are compatible with each other. The present invention proposes a solution for the problem as described above in order to fermentatively produce L-lysine by using a coryneform bacterium.

The principle of the present invention is based on the fact that the growth of a coryneform bacterium can be improved, and the L-lysine-producing speed thereof can be improved by enhancing both of a DNA sequence coding for an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and a DNA sequence coding for a diaminopimelate decarboxylase compared with the case in which these DNA sequences are each enhanced singly.

In a first aspect of the present invention, it is provided a recombinant DNA autonomously replicable in cells of coryneform bacteria, comprising a DNA sequence coding for an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and a DNA sequence coding for a diaminopimelate decarboxylase. The recombinant DNA further comprising a DNA sequence coding for a phosphoenolpyruvate carboxylase is also provided.

In a second aspect of the present invention, it is provided a coryneform bacterium harboring an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and comprising an enhanced DNA sequence coding for a diaminopimelate decarboxylase. The coryneform bacterium further comprising an enhanced DNA sequence coding for a phosphoenolpyruvate carboxylase is also provided.

In a third aspect of the present invention, it is provided a method for producing L-lysine comprising the steps of cultivating any of coryneform bacteria as described in the above in an appropriate medium to allow L-lysine to be produced and accumulated in a culture of the bacterium, and collecting L-lysine from the culture.

Hereinafter, an aspartokinase is referred to as "AK", a gene coding for AK is referred to as "lysC", AK which is desensitized in feedback inhibition by L-lysine and L-threonine is referred to as "mutant AK", and a gene coding for mutant AK is referred to as "mutant lysC", if necessary. Also, a diaminopimelate decarboxylase is referred to as "DDC", a gene coding for DDC is referred to as "lysA", a phosphoenolpyruvate carboxylase is referred to as "PEPC", and a gene coding for PEPC is referred to as "ppc", if necessary.

The coryneform bacteria referred to in the present invention are a group of microorganisms as defined in Bergey's Manual of Determinative Bacteriology, 8th ed., p. 599 (1974), which are aerobic Gram-positive non-acid-fast rods having no spore-forming ability. The coryneform bacteria include bacteria belonging to the genus Corynebacterium, bacteria belonging to the genus Brevibacterium having been hitherto classified into the genus Brevibacterium but united as bacteria belonging to the genus Corynebacterium at present, and bacteria belonging to the genus Brevibacterium closely relative to bacteria belonging to the genus Corynebacterium.

According to the present invention, a production amount and a production speed of L-lysine of coryneform bacteria can be improved.

BRIEF EXPLANATION OF THE DRAWINGS

- Fig. 1 illustrates a process of construction of plasmids p399AK9B and p399AKYB comprising mutant lysC.
 Fig. 2 illustrates a process of construction of a plasmid p299LYSA comprising lysA.
 Fig. 3 illustrates a process of construction of a plasmid pLYSAB comprising lysA and Brevi.-ori.
 Fig. 4 illustrates a process of construction of a plasmid pAKPFds comprising a PEPC structural gene.
 Fig. 5 illustrates a process of construction of novel cloning vectors for Coryneform bacteria, pVK6 and pVK7.
 Fig. 6 illustrates a process of construction of a plasmid pPwm comprising a wild type high expression ppc.
 Fig. 7 illustrates a process of construction of a plasmid pCL comprising mutant lysC, lysA and Brevi.-ori.
 Fig. 8 illustrates a process of construction of a plasmid pDPSB comprising dapA and Brevi.-ori.
 Fig. 9 illustrates a process of construction of a plasmid pDPRB comprising dapB and Brevi.-ori.
 Fig. 10 illustrates a process of construction of a plasmid pPK4D comprising ddh and Brevi.-ori.
 Fig. 11 illustrates a process of construction of a plasmid pCRCAB comprising lysC, dapA and Brevi.-ori.
 Fig. 12 illustrates a process of construction of a plasmid pCB comprising mutant lysC, dapB, and Brevi.-ori.
 Fig. 13 illustrates a process of construction of a plasmid pCD comprising mutant lysC and ddh.

DETAILED DESCRIPTION OF THE INVENTION

(1) Preparation of genes for L-lysine biosynthesis used for the present invention

The genes for L-lysine biosynthesis used in the present invention are obtained respectively by preparing chromosomal DNA from a bacterium as a DNA donor, constructing a chromosomal DNA library by using a plasmid vector or the like, selecting a strain harboring a desired gene, and recovering, from the selected strain, recombinant DNA into which the gene has been inserted. The DNA donor for the gene for L-lysine biosynthesis used in the present invention is not specifically limited provided that the desired gene for L-lysine biosynthesis expresses an enzyme protein which functions in cells of coryneform bacteria. However, the DNA donor is preferably a coryneform bacterium.

All of the genes of lysC, dapA, and ppc originating from coryneform bacteria have known sequences. Accordingly, they can be obtained by performing amplification in accordance with the polymerase chain reaction method (PCR; see White, T. J. et al., Trends Genet., 5, 185 (1989)).

Each of the genes for L-lysine biosynthesis used in the present invention is obtainable in accordance with certain methods as exemplified below.

(1) Preparation of mutant lysC

A DNA fragment containing mutant lysC can be prepared from a mutant strain in which synergistic feedback inhibition on the AK activity by L-lysine and L-threonine is substantially desensitized (International Publication Pamphlet of WO 94/25605). Such a mutant strain can be obtained, for example, from a group of cells originating from a wild type

strain of a coryneform bacterium subjected to a mutation treatment by applying an ordinary mutation treatment such as ultraviolet irradiation and treatment with a mutagenic agent such as N-methyl-N'-nitro-N-nitrosoguanidine (NTG). The AK activity can be measured by using a method described by Miyajima, R. et al. in The Journal of Biochemistry (1968), 63(2), 139-148. The most preferred as such a mutant strain is represented by an L-lysine-producing bacterium AJ3445 (FERM P-1944) derived by a mutation treatment from a wild type strain of Brevibacterium lactofermentum ATCC 13869 (having its changed present name of Corynebacterium glutamicum).

Alternatively, mutant lysC is also obtainable by an in vitro mutation treatment of plasmid DNA containing wild type lysC. In another aspect, information is specifically known on mutation to desensitize synergistic feedback inhibition on AK by L-lysine and L-threonine (International Publication Pamphlet of WO 94/25605). Accordingly, mutant lysC can be also prepared from wild type lysC on the basis of the information in accordance with, for example, the site-directed mutagenesis method.

A fragment comprising lysC can be isolated from a coryneform bacterium by preparing chromosomal DNA in accordance with, for example, a method of Saito and Miura (H. Saito and K. Miura, Biochem. Biophys. Acta, 72, 619 (1963)), and amplifying lysC in accordance with the polymerase chain reaction method (PCR; see White, T. J. et al., Trends Genet., 5, 185 (1989)).

DNA primers are exemplified by single strand DNA's of 23-mer and 21-mer having nucleotide sequences shown in SEQ ID NOs: 1 and 2 in Sequence Listing in order to amplify, for example, a region of about 1,643 bp coding for lysC based on a sequence known for Corynebacterium glutamicum (see Molecular Microbiology (1991), 5(5), 1197-1204; Mol. Gen. Genet. (1990), 224, 317-324). DNA can be synthesized in accordance with an ordinary method by using DNA synthesizer model 380B produced by Applied Biosystems and using the phosphoramidite method (see Tetrahedron Lett. (1981), 22, 1859). PCR can be performed by using DNA Thermal Cycler Model PJ2000 produced by Takara Shuzo, and using Taq DNA polymerase in accordance with a method designated by the supplier.

It is preferred that lysC amplified by PCR is ligated with vector DNA autonomously replicable in cells of E. coli and/or coryneform bacteria to prepare recombinant DNA, and the recombinant DNA is introduced into cells of E. coli beforehand. Such provision makes following operations easy. The vector autonomously replicable in cells of E. coli is preferably a plasmid vector which is preferably autonomously replicable in cells of a host, including, for example, pUC19, pUC18, pBR322, pHSG299, pHSG399, pHSG398, and RSF1010.

When a DNA fragment having an ability to allow a plasmid to be autonomously replicable in coryneform bacteria is inserted into these vectors, they can be used as a so-called shuttle vector autonomously replicable in both E. coli and coryneform bacteria.

Such a shuttle vector includes the followings. Microorganisms harboring each of vectors and accession numbers in international deposition authorities (in parentheses) are shown.

pHC4: Escherichia coli AJ12617 (FERM BP-3532)
 pAJ655: Escherichia coli AJ11882 (FERM BP-136) Corynebacterium glutamicum SR8201 (ATCC 39135)
 pAJ1844: Escherichia coli AJ11883 (FERM BP-137) Corynebacterium glutamicum SR8202 (ATCC 39136)
 pAJ611: Escherichia coli AJ11884 (FERM BP-138)
 pAJ3148: Corynebacterium glutamicum SR8203 (ATCC 39137)
 pAJ440: Bacillus subtilis AJ11901 (FERM BP-140)

These vectors are obtainable from the deposited microorganisms as follows. Cells collected at a logarithmic growth phase were lysed by using lysozyme and SDS, followed by separation from a lysate by centrifugation at 30,000 × g to obtain a supernatant. To the supernatant, polyethylene glycol is added, followed by fractionation and purification by means of cesium chloride-ethidium bromide equilibrium density gradient centrifugation.

E. coli can be transformed by introducing a plasmid in accordance with, for example, a method of D. M. Morrison (Methods in Enzymology, 68, 326 (1979)) or a method in which recipient cells are treated with calcium chloride to increase permeability for DNA (Mandel, M. and Higa, A., J. Mol. Biol., 53, 159 (1970)).

Wild type lysC is obtained when lysC is isolated from an AK wild type strain, while mutant lysC is obtained when lysC is isolated from an AK mutant strain in accordance with the method as described above.

An example of a nucleotide sequence of a DNA fragment containing wild type lysC is shown in SEQ ID NO: 3 in Sequence Listing. An amino acid sequence of α -subunit of a wild type AK protein is deduced from the nucleotide sequence, and is shown in SEQ ID NO: 4 in Sequence Listing together with the DNA sequence. Only the amino acid sequence is shown in SEQ ID NO: 5. An amino acid sequence of β -subunit of the wild type AK protein is deduced from the nucleotide sequence of DNA, and is shown in SEQ ID NO: 6 in Sequence Listing together with the DNA sequence. Only the amino acid sequence is shown in SEQ ID NO: 7. In each of the subunits, GTG is used as an initiation codon, and a corresponding amino acid is represented by methionine. However, this representation refers to methionine, valine, or formylmethionine.

The mutant lysC used in the present invention is not specifically limited provided that it codes for AK in which syn-

ergistic feedback inhibition by L-lysine and L-threonine is desensitized. However, the mutant lysC is exemplified by one including mutation in which an amino acid residue corresponding to a 279th alanine residue as counted from the N-terminal is changed into an amino acid residue other than alanine and other than acidic amino acid in the α -subunit, and an amino acid residue corresponding to a 30th alanine residue from the N-terminal is changed into an amino acid residue other than alanine and other than acidic amino acid in the β -subunit in the amino acid sequence of the wild type AK. The amino acid sequence of the wild type AK specifically includes the amino acid sequence shown in SEQ ID NO: 5 in Sequence Listing as the α -subunit, and the amino acid sequence shown in SEQ ID NO: 7 in Sequence Listing as the β -subunit.

Those preferred as the amino acid residue other than alanine and other than acidic amino acid include threonine, arginine, cysteine, phenylalanine, proline, serine, tyrosine, and valine residues.

The codon corresponding to an amino acid residue to be substituted is not specifically limited for its type provided that it codes for the amino acid residue. It is predicted that the amino acid sequence of wild type AK may slightly differ depending on the difference in bacterial species and bacterial strains. AK's, which have mutation based on, for example, substitution, deletion, or insertion of one or more amino acid residues at one or more positions irrelevant to the enzyme activity as described above, can be also used for the present invention. A DNA coding for AK having the spontaneous mutation can be obtained by isolating a DNA which is hybridizable with, for example, the DNA having a part of the nucleotide sequence shown in SEQ ID NO: 3 under the stringent condition. By the "stringent condition" referred to herein is meant a condition under which a specific hybrid is formed, and nonspecific hybrid is not formed. It is difficult to clearly express the condition with numerical values. However, the condition is exemplified by a condition under which, nucleic acid having high homology, for example, DNA's having homology of not less than 90% are hybridized with each other, and nucleic acids having homology lower than the above are not hybridized with each other, or a condition of a temperature of from a melting out temperature (T_m) of a completely-matched hybrid to ($T_m - 30$) °C, preferably from T_m to ($T_m - 20$) °C and a salt concentration corresponding to $1 \times$ SSC, preferably $0.1 \times$ SSC.

Other AK's, which have artificial mutation based on, for example, substitution, deletion, or insertion of other one or more amino acid residues, can be also used provided that no influence is substantially exerted on the AK activity, and on the desensitization of synergistic feedback inhibition by L-lysine and L-threonine. A DNA coding for AK having the artificial mutation can be obtained by modifying the nucleotide sequence to give substitution, deletion or insertion of a specified site by, for example, site-specific mutagenesis. Also, lysC having the mutation can be obtained by known mutagen treatment. The mutagen treatment includes in vitro treatment of a DNA containing lysC with hydroxylamine or the like, and treatment of microorganism harboring a DNA containing lysC with a mutagen such as ultraviolet irradiation or a mutagenic agent used for ordinary artificial mutagenesis such as N-methyl-N'-nitro-N-nitrosoguanidine (NTG) or nitric acid. After the mutagen treatment, a site to which mutation is introduced or in which mutation occurs can be determined by selecting a DNA or a microorganism which codes for or produces AK which has the AK activity and whose amino acid sequence is mutated from the DNA subjected to the mutagen treatment or the microorganism subjected to the mutagen treatment. A site of the introduced mutation is not specifically restricted provided that no influence is substantially exerted on the AK activity and on densitization of feedback inhibition. A number of the introduced mutation varies depending on a site or a kind of the mutated amino acid in a steric structure of a protein, and is not specifically restricted provided that no influence is substantially exerted on the AK activity and on densitization of feedback inhibition. The number is usually 1 to 20, preferably 1 to 10.

An AJ12691 strain obtained by introducing a mutant lysC plasmid p399AK9B into an AJ12036 strain (FERM BP-734) as a wild type strain of Brevibacterium lactofermentum has been deposited on April 10, 1992 under an accession number of FERM P-12918 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology of Ministry of International Trade and Industry (1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, 305 Japan), transferred to international deposition based on the Budapest Treaty on February 10, 1995, and deposited under an accession number of FERM BP-4999.

(2) Preparation of lysA

A DNA fragment containing lysA can be prepared from chromosome of a coryneform bacterium by means of PCR. The DNA donor is not specifically limited, however, it is exemplified by Brevibacterium lactofermentum ATCC 13869 strain.

In the coryneform bacteria, lysA forms an operon together with argS (arginyl-tRNA synthase gene), and lysA exists downstream from argS. Expression of lysA is regulated by a promoter existing upstream from argS (see Journal of Bacteriology, Nov., 7356-7362 (1993)). DNA sequences of these genes are known for Corynebacterium glutamicum (see Molecular Microbiology, 4(11), 1819-1830 (1990); Molecular and General Genetics, 212, 112-119 (1988)), on the basis of which DNA primers for PCR can be prepared. Such DNA primers are specifically exemplified by DNA's of 23-mers respectively having nucleotide sequences shown in SEQ ID NO: 8 in Sequence Listing (corresponding to nucleotide numbers 11 to 33 in a nucleotide sequence described in Molecular Microbiology, 4(11), 1819-1830 (1990)) and SEQ ID

NO: 9 (corresponding to nucleotide numbers 1370 to 1392 in a nucleotide sequence described in Molecular and General Genetics, 212, 112-119 (1988)). Synthesis of DNA, PCR, and preparation of a plasmid containing obtained lysA can be performed in the same manner as those for lysC described above.

In Example described later on, a DNA fragment containing a promoter, argS, and lysA was used in order to enhance lysA. However, argS is not essential for the present invention. It is allowable to use a DNA fragment in which lysA is ligated just downstream from a promoter.

A nucleotide sequence of a DNA fragment containing argS and lysA, and an amino acid sequence deduced to be encoded by the nucleotide sequence are exemplified in SEQ ID NO: 10. An example of an amino acid sequence encoded by argS is shown in SEQ ID NO: 11, and an example of an amino acid sequence encoded by lysA is shown in SEQ ID NO: 12. In addition to DNA fragments coding for these amino acid sequences, the present invention can equivalently use DNA fragments coding for amino acid sequences substantially the same as the amino acid sequence shown in SEQ ID NO: 12, namely amino acid sequences having mutation based on, for example, substitution, deletion, or insertion of one or more amino acids provided that there is no substantial influence on the DDC activity. The lysA having spontaneous or artificial mutation can be obtained in the same manner as those for the DNA coding for AK having mutation which exerts no influence on the AK activity and on the desensitization of synergistic feedback inhibition by L-lysine and L-threonine.

(3) Preparation of ppc

A DNA fragment containing ppc can be prepared from chromosome of a coryneform bacterium by means of PCR. The DNA donor is not specifically limited, however, it is exemplified by Brevibacterium lactofermentum ATCC 13869 strain.

A DNA sequences of the ppc gene is known for Corynebacterium glutamicum (see O'Regan, M. et al., Gene, 77, 237-251 (1989)), on the basis of which DNA primers for PCR can be prepared. Such DNA primers are specifically exemplified by DNA's of 23-mers respectively having nucleotide sequences shown in SEQ ID NOs: 13 and 14 in Sequence Listing. Synthesis of DNA, PCR, and preparation of a plasmid containing obtained ppc can be performed in the same manner as those for lysC described above.

A nucleotide sequence of a DNA fragment containing ppc, and an amino acid sequence deduced to be encoded by the nucleotide sequence are shown in SEQ ID NO: 15. Only the amino acid sequence is shown in SEQ ID NO: 16.

In addition to DNA fragments coding for these amino acid sequences, the present invention can equivalently use DNA fragments coding for amino acid sequences substantially the same as the amino acid sequence shown in SEQ ID NO: 16, namely amino acid sequences having mutation based on, for example, substitution, deletion, or insertion of one or more amino acids provided that there is no substantial influence on the PEPC activity. The ppc having spontaneous or artificial mutation can be obtained in the same manner as those for the DNA coding for AK having mutation which exerts no influence on the AK activity and on the desensitization of synergistic feedback inhibition by L-lysine and L-threonine.

The ppc from the coryneform bacteria forms an operon together with gap (glyceraldehyde-3-phosphate dehydrogenase gene), pgk (phosphoglycerate kinase gene) and tpi (triose phosphate isomerase gene), and ppc exists downstream from tpi. Expression of ppc is regulated by a promoter existing upstream from pgk (see Schwinde, J.W. et al., J. Bacteriol., 175(12), 3905-3908 (1993)). Therefore, like the above-mentioned lysA, ppc can be amplified together with pgk and tpi by PCR to use a DNA fragment containing pgk, tpi and ppc. As shown in Example described later on, it is allowable to use a DNA fragment in which a suitable promoter is ligated just upstream from a coding region of PEPC. The promoter includes a promoter of lysC, tac promoter originating from E. coli, and trc promoter.

(2) Recombinant DNA and coryneform bacterium of the present invention

The recombinant DNA comprises a DNA sequence coding for an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and a DNA sequence coding for a diaminopimelate decarboxylase, and is autonomously replicable in cells of coryneform bacteria. In a preferred embodiment, the recombinant DNA further comprises a DNA sequence coding for a phosphoenolpyruvate carboxylase in addition to the above DNA sequences.

The coryneform bacterium of the present invention harbors an aspartokinase (mutant AK) in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, wherein DNA (lysA) coding for a diaminopimelate decarboxylase is enhanced. In a preferred embodiment, the coryneform bacterium of the present invention is a coryneform bacterium in which DNA (ppc) coding for a phosphoenolpyruvate carboxylase is further enhanced.

The term "enhance" herein refers to the fact that the intracellular activity of an enzyme encoded by the DNA is raised by, for example, increasing the copy number of a gene, using a strong promoter, using a gene coding for an enzyme having a high specific activity, or combining these means.

The coryneform bacterium harboring the mutant AK may be those which produce the mutant aspartokinase as a result of mutation, or those which are transformed by introducing mutant lysC.

Examples of the coryneform bacterium used to introduce the DNA described above include, for example, the following lysine-producing wild type strains: Corynebacterium acetoacidophilum ATCC 13870; Corynebacterium acetoglutamicum ATCC 15806; Corynebacterium callunae ATCC 15991; Corynebacterium glutamicum ATCC 13032; (5) Brevibacterium divaricatum ATCC 14020; (Brevibacterium lactofermentum) ATCC 13869; (Corynebacterium lilium) ATCC 15990; (Brevibacterium flavum) ATCC 14067; Corynebacterium melassecola ATCC 17965; Brevibacterium saccharolyticum ATCC 14066; Brevibacterium immariophilum ATCC 14068; Brevibacterium roseum ATCC 13825; Brevibacterium thiogenitalis ATCC 19240; Microbacterium ammoniaphilum ATCC 15354; Corynebacterium (10) thermoaminogenes AJ12340 (FERM BP-1539).

Other than the bacterial strains described above, those usable as a host include, for example, mutant strains having an L-lysine-producing ability derived from the aforementioned strains. Such artificial mutant strains includes the follow- ings: S-(2-aminoethyl)-cysteine (hereinafter abbreviated as "AEC") resistant mutant strains (for example, Brevibacte- (15) rium lactofermentum AJ11082 (NRRL B-1147), Japanese Patent Publication Nos. 56-1914, 56-1915, 57-14157, 57-14158, 57-30474, 58-10075, 59-4993, 61-35840, 62-24074, 62-36673, 5-11958, 7-112437, and 7-112438); mutant strains which require amino acid such as L-homoserine for their growth (Japanese Patent Publication Nos. 48-28078 and 56-6499); mutant strains which exhibit resistance to AEC and require amino acids such as L-leucine, L-homoserine, L-proline, L-serine, L-arginine, L-alanine, and L-valine (United States Patent Nos. 3,708,395 and 3,825,472); L-lysine-producing mutant strains which exhibit resistance to DL- α -amino- ϵ -caprolactam, α -amino-lauryllactam, aspartate-analog, sulfa drug, quinoid, and N-lauroylleucine; L-lysine-producing mutant strains which exhibit resistance to inhibitors of oxaloacetate decarboxylase or respiratory system enzymes (Japanese Patent Application Laid-open Nos. 50-53588, 50-31093, 52-102498, 53-9394, 53-86089, 55-9783, 55-9759, 56-32995 and 56-39778, and Japanese Pat- (20) ent Publication Nos. 53-43591 and 53-1833); L-lysine-producing mutant strains which require inositol or acetic acid (Japanese Patent Application Laid-open Nos. 55-9784 and 56-8692); L-lysine-producing mutant strains which exhibit (25) sensitivity to fluoropyruvic acid or temperature not less than 34°C (Japanese Patent Application Laid-open Nos. 55-9783 and 53-86090); and producing mutant strains belonging to the genus Brevibacterium or Corynebacterium which exhibit resistance to ethylene glycol and produce L-lysine (United States Patent No. 4,411,997).

In a specified embodiment, in order to enhance the genes for L-lysine biosynthesis in the host as described above, the genes are introduced into the host by using a plasmid vector, transposon or phage vector or the like. Upon the intro- (30) duction, it is expected to make enhancement to some extent even by using a low copy type vector. However, it is preferred to use a multiple copy type vector. Such a vector includes, for example, plasmid vectors, pAJ655, pAJ1844, pAJ611, pAJ3148, and pAJ440 described above. Besides, transposons derived from coryneform bacteria are described in International Publication Pamphlets of WO02/02627 and WO93/18151, European Patent Publication No. 445385, Japanese Patent Application Laid-open No. 6-46867, Vertes, A. A. et al., Mol. Microbiol., 11, 739-746 (1994), (35) Bonamy, C., et al., Mol. Microbiol., 14, 571-581 (1994), Vertes, A. A. et al., Mol. Gen. Genet., 245, 397-405 (1994), Jagar, W. et al., FEMS Microbiology Letters, 126, 1-6 (1995), Japanese Patent Application Laid-open No. 7-107976, Japanese Patent Application Laid-open No. 7-327680 and the like.

In the present invention, it is not indispensable that the mutant lysC is necessarily enhanced. It is allowable to use those which have mutation on lysC on chromosomal DNA, or in which the mutant lysC is incorporated into chromo- (40) somal DNA. Alternatively, the mutant lysC may be introduced by using a plasmid vector. On the other hand, lysA and ppc are preferably enhanced in order to efficiently produce L-lysine.

Each of the genes of lysC, lysA, and ppc may be successively introduced into the host by using different vectors respectively. Alternatively, two or three species of the genes may be introduced together by using a single vector. When (45) different vectors are used, the genes may be introduced in any order, however, it is preferred to use vectors which have a stable sharing and harboring mechanism in the host, and which are capable of co-existing with each other.

A coryneform bacterium harboring the mutant AK and further comprising enhanced lysA is obtained, for example, by introducing, into a host coryneform bacterium, a recombinant DNA containing mutant lysC, lysA and ppc auton- (50) omously replicable in cells of coryneform bacteria.

A coryneform bacterium further comprising enhanced ppc in addition to mutant lysC and lysA is obtained, for exam- (50) ple, by introducing, into a host coryneform bacterium, a recombinant DNA containing mutant lysC, lysA, and ppc auton- omously replicable in cells of coryneform bacteria. Also, a coryneform bacterium comprising enhanced mutant lysC, lysA and ppc is obtained by introducing, into a coryneform bacterium comprising enhanced mutant lysC and lysA, a recombinant DNA containing ppc autonomously replicable in cells of coryneform bacteria.

The above-mentioned recombinant DNAs can be obtained, for example, by inserting each of the genes participat- (55) ing in L-lysine biosynthesis into a vector such as plasmid vector, transposon or phage vector as described above.

In the case in which a plasmid is used as a vector, the recombinant DNA can be introduced into the host in accord- (55) ance with an electric pulse method (Sugimoto et al., Japanese Patent Application Laid-open No. 2-207791). Amplifica- tion of a gene using transposon can be performed by introducing a plasmid which carrying a transposon into the host

cell and inducing transposition of the transposon.

(3) Method for producing L-lysine

L-Lysine can be efficiently produced by cultivating, in an appropriate medium, the coryneform bacterium comprising the enhanced genes for L-lysine biosynthesis as described above, to allow L-lysine to be produced and accumulated in a culture of the bacterium, and collecting L-lysine from the culture.

The medium to be used is exemplified by an ordinary medium containing a carbon source, a nitrogen source, inorganic ions, and optionally other organic components.

As the carbon source, it is possible to use sugars such as glucose, fructose, sucrose, molasses, and starch hydrolysate; and organic acids such as fumaric acid, citric acid, and succinic acid.

As the nitrogen source, it is possible to use inorganic ammonium salts such as ammonium sulfate, ammonium chloride, and ammonium phosphate; organic nitrogen such as soybean hydrolysate; ammonia gas; and aqueous ammonia.

As organic trace nutrient sources, it is desirable to contain required substances such as vitamin B₁ and L-homoserine or yeast extract or the like in appropriate amounts. Other than the above, potassium phosphate, magnesium sulfate, iron ion, manganese ion and so on are added in small amounts, if necessary.

Cultivation is preferably carried out under an aerobic condition for about 30 to 90 hours. The cultivation temperature is preferably controlled at 25°C to 37°C, and pH is preferably controlled at 5 to 8 during cultivation. Inorganic or organic, acidic or alkaline substances, or ammonia gas or the like can be used for pH adjustment. L-lysine can be collected from a culture by combining an ordinary ion exchange resin method, a precipitation method, and other known methods.

Examples

The present invention will be more specifically explained below with reference to Examples.

Example 1: Preparation of Wild Type *lysC* Gene and Mutant *lysC* Gene from *Brevibacterium lactofermentum*

(1) Preparation of wild type and mutant *lysC*'s and preparation of plasmids containing them

A strain of *Brevibacterium lactofermentum* ATCC 13869, and an L-lysine-producing mutant strain AJ3445 (FERM P-1944) obtained from the ATCC 13869 strain by a mutation treatment were used as chromosomal DNA donors. The AJ3445 strain had been subjected to mutation so that *lysC* was changed to involve substantial desensitization from concerted inhibition by lysine and threonine (*Journal of Biochemistry*, 68, 701-710 (1970)).

A DNA fragment containing *lysC* was amplified from chromosomal DNA in accordance with the PCR method (polymerase chain reaction; see White, T. J. et al., *Trends Genet.*, 5, 185 (1989)). As for DNA primers used for amplification, single strand DNA's of 23-mer and 21-mer having nucleotide sequences shown in SEQ ID NOs: 1 and 2 were synthesized in order to amplify a region of about 1,643 bp coding for *lysC* on the basis of a sequence known for *Corynebacterium glutamicum* (see *Molecular Microbiology* (1991), 5(5), 1197-1204; and *Mol. Gen. Genet.* (1990), 224, 317-324). DNA was synthesized in accordance with an ordinary method by using DNA synthesizer model 380B produced by Applied Biosystems and using the phosphoramidite method (see *Tetrahedron Letters* (1981), 22, 1859).

The gene was amplified by PCR by using DNA Thermal Cycler Model PJ2000 produced by Takara Shuzo, and using Taq DNA polymerase in accordance with a method designated by the supplier. An amplified gene fragment of 1,643 kb was confirmed by agarose gel electrophoresis. After that, the fragment excised from the gel was purified in accordance with an ordinary method, and it was digested with restriction enzymes *Nru*I (produced by Takara Shuzo) and *Eco*RI (produced by Takara Shuzo).

pHSG399 (see Takeshita, S. et al., *Gene* (1987), 61, 63-74) was used as a cloning vector for the gene fragment. pHSG399 was digested with restriction enzymes *Sma*I (produced by Takara Shuzo) and *Eco*RI, and it was ligated with the amplified *lysC* fragment. DNA was ligated by using DNA ligation kit (produced by Takara Shuzo) in accordance with a designated method. Thus plasmids were prepared, in which the *lysC* fragments amplified from chromosomes of *Brevibacterium lactofermentum* were ligated with pHSG399 respectively. A plasmid comprising *lysC* from ATCC 13869 (wild type strain) was designated as p399AKY, and a plasmid comprising *lysC* from AJ3463 (L-lysine-producing bacterium) was designated as p399AK9.

A DNA fragment (hereinafter referred to as "Brevi.-ori") having an ability to make a plasmid autonomously replicable in bacteria belonging to the genus *Corynebacterium* was introduced into p399AKY and p399AK9 respectively to prepare plasmids carrying *lysC* autonomously replicable in bacteria belonging to the genus *Corynebacterium*. Brevi.-ori was prepared from a plasmid vector pHK4 containing Brevi.-ori and autonomously replicable in cells of both *Escherichia coli* and bacteria belonging to the genus *Corynebacterium*. pHK4 was constructed by digesting pHK4 with *Kpn*I (produced by Takara Shuzo) and *Bam*HI (produced by Takara Shuzo), extracting a Brevi.-ori fragment, and ligating

it with pHSG298 having been also digested with KpnI and BamHI (see Japanese Patent Application Laid-open No. 5-7491). pHK4 gives kanamycin resistance to a host. Escherichia coli harboring pHK4 was designated as Escherichia coli AJ13136, and deposited on August 1, 1995 under an accession number of FERM BP-5186 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology of Ministry of International Trade and Industry (1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, 305 Japan).

pHK4 was digested with restriction enzymes KpnI and BamHI, and cleaved edges were blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method. After the blunt end formation, a phosphorylated BamHI linker (produced by Takara Shuzo) was ligated to make modification so that the DNA fragment corresponding to the Brevi.-ori portion might be excised from pHK4 by digestion with only BamHI. This plasmid was digested with BamHI, and the generated Brevi.-ori DNA fragment was ligated with p399AKY and p399AK9 having been also digested with BamHI respectively to prepare plasmids each containing the lysC gene autonomously replicable in bacteria belonging to the genus Corynebacterium.

A plasmid containing the wild type lysC gene originating from p399AKY was designated as p399AKYB, and a plasmid containing the mutant lysC gene originating from p399AK9 was designated as p399AK9B. The process of construction of p399AK9B and p399AKYB is shown in Fig. 1. A strain AJ12691 obtained by introducing the mutant lysC plasmid p399AK9B into a wild type strain of Brevibacterium lactofermentum (AJ12036 strain, FERM BP-734) was deposited on April 10, 1992 under an accession number of FERM P-12918 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology of Ministry of International Trade and Industry (1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, 305 Japan), transferred to international deposition based on the Budapest Treaty on February 10, 1995, and deposited under an accession number of FERM BP-4999.

(2) Determination of nucleotide sequences of wild type lysC and mutant lysC from Brevibacterium lactofermentum

The plasmid p399AKY containing the wild type lysC and the plasmid p399AK9 containing the mutant lysC were prepared from the respective transformants to determine nucleotide sequences of the wild type and mutant lysC's. Nucleotide sequence determination was performed in accordance with a method of Sanger et al. (for example, F. Sanger et al., Proc. Natl. Acad. Sci., 74, 5463 (1977)).

The nucleotide sequence of wild type lysC encoded by p399AKY is shown in SEQ ID NO: 3 in Sequence Listing. On the other hand, the nucleotide sequence of mutant lysC encoded by p399AK9 had only mutation of one nucleotide such that 1051st G was changed into A in SEQ ID NO: 3 as compared with wild type lysC. It is known that lysC of Corynebacterium glutamicum has two subunits (α , β) encoded in an identical reading frame on an identical DNA strand (see Kalinowski, J. et al., Molecular Microbiology (1991) 5(5), 1197-1204). Judging from homology, it is assumed that the gene sequenced herein also has two subunits (α , β) encoded in an identical reading frame on an identical DNA strand.

An amino acid sequence of the α -subunit of the wild type AK protein deduced from the nucleotide sequence of DNA is shown in SEQ ID NO: 4 together with the DNA sequence. Only the amino acid sequence is shown in SEQ ID NO: 5. An amino acid sequence of the β -subunit of the wild type AK protein deduced from the nucleotide sequence of DNA is shown in SEQ ID NO: 6 together with DNA sequence. Only the amino acid sequence is shown in SEQ ID NO: 7. In each of the subunits, GTG is used as an initiation codon, and a corresponding amino acid is represented by methionine. However, this representation refers to methionine, valine, or formylmethionine.

On the other hand, mutation on the sequence of mutant lysC means occurrence of amino acid residue substitution such that a 279th alanine residue of the α -subunit is changed into a threonine residue, and a 30th alanine residue of the β -subunit is changed into a threonine residue in the amino acid sequence of the wild type AK protein (SEQ ID NOs: 5, 7).

Example 2: Preparation of lysA from Brevibacterium lactofermentum

(1) Preparation of lysA and construction of plasmid containing lysA

A wild type strain of Brevibacterium lactofermentum ATCC 13869 was used as a chromosomal DNA donor. Chromosomal DNA was prepared from the ATCC 13869 strain in accordance with an ordinary method. A DNA fragment containing argS, lysA, and a promoter of an operon containing them was amplified from the chromosomal DNA in accordance with PCR. As for DNA primers used for amplification, synthetic DNA's of 23-mers having nucleotide sequences shown in SEQ ID NOs: 8 and 9 in Sequence Listing respectively were used in order to amplify a region of about 3.6 kb coding for arginyl-tRNA synthase and DDC on the basis of a sequence known for Corynebacterium glutamicum (see Molecular Microbiology, 4(11), 1819-1830 (1990); Molecular and General Genetics, 212, 112-119 (1988)). Synthesis of DNA and PCR were performed in the same manner as described in Example 1. pHSG399 was used as a cloning vector for the amplified gene fragment of 3,579 bp. pHSG399 was digested with a restriction enzyme

SmaI (produced by Takara Shuzo), and was ligated with the DNA fragment containing amplified lysA. A plasmid obtained as described above, which had lysA originating from ATCC 13869, was designated as p399LYSA.

A DNA fragment containing lysA was extracted by digesting p399LYSA with KpnI (produced by Takara Shuzo) and BamHI (produced by Takara Shuzo). This DNA fragment was ligated with pHSG299 having been digested with KpnI and BamHI. An obtained plasmid was designated as p299LYSA. The process of construction of p299LYSA is shown in Fig. 2.

Brevi.-ori was introduced into the obtained p299LYSA to construct a plasmid carrying lysA autonomously replicable in coryneform bacteria. pHK4 was digested with restriction enzymes KpnI and BamHI, and cleaved edges were blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method. After the blunt end formation, a phosphorylated KpnI linker (produced by Takara Shuzo) was ligated to make modification so that the DNA fragment corresponding to the Brevi.-ori portion might be excised from pHK4 by digestion with only KpnI. This plasmid was digested with KpnI, and the generated Brevi.-ori DNA fragment was ligated with p299LYSA having been also digested with KpnI to prepare a plasmid containing lysA autonomously replicable in coryneform bacteria. The prepared plasmid was designated as pLYSAB. The process of construction of pLYSAB is shown in Fig. 3.

(2) Determination of nucleotide sequence of lysA from Brevibacterium lactofermentum

Plasmid DNA of p299LYSA was prepared, and its nucleotide sequence was determined in the same manner as described in Example 1. A determined nucleotide sequence and an amino acid sequence deduced to be encoded by the nucleotide sequence are shown in SEQ ID NO: 10. Concerning the nucleotide sequence, an amino acid sequence encoded by argS and an amino acid sequence encoded by lysA are shown in SEQ ID NOs: 11 and 12, respectively.

Example 3: Preparation of ppc from Brevibacterium lactofermentum

(1) Preparation of ppc

A wild type strain of Brevibacterium lactofermentum ATCC 13869 was used as a chromosomal DNA donor. Chromosomal DNA was prepared from the ATCC 13869 strain in accordance with an ordinary method. A DNA fragment containing ppc was amplified from the chromosomal DNA in accordance with PCR. As for DNA primers used for amplification, synthetic DNA's of 23-mers having nucleotide sequences shown in SEQ ID NOs: 13 and 14 in Sequence Listing respectively were used in order to amplify a region of about 3.3 kb coding for PEPC on the basis of a sequence known for Corynebacterium glutamicum (see O'Regan, M. et al., Gene, 77, 237-251 (1989)). Synthesis of DNA and PCR were performed in the same manner as described in Example 1.

An amplified gene fragment of about 3,300 bp was confirmed by agarose gel electrophoresis, and then the fragment extracted from the gel was purified by an ordinary method and digested with a restriction enzyme SalI (produced by Takara Shuzo). pHSG399 was used as a cloning vector for ppc. pHSG399 was digested with a restriction enzyme SalI (produced by Takara Shuzo), and was ligated with the DNA fragment containing amplified ppc. A plasmid obtained as described above, which had ppc originating from ATCC 13869, was designated as pPCF.

(2) Ligation of ppc gene with lysC promoter

The pPCF obtained as described in the above was digested with a restriction enzyme DraI (produced by Takara Shuzo). After a DNA fragment of about 150 bp upstream of the PEPC structural gene was removed, self-ligation was effected to obtain a plasmid pPCFDs. pPCFDs was digested with a restriction enzyme SalI (produced by Takara Shuzo), and cleaved edges were blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method.

p399AKYB containing wild type lysC obtained in Example 1 was digested with restriction enzymes ApaLI and PstII (both produced by Takara Shuzo), and cleaved edges were blunt-ended in the same manner as above. A smaller fragment among the obtained two DNA fragments contains Brevi.-ori and a promoter of lysC. This fragment was ligated with the above-mentioned fragment obtained by digesting pPCFDs with SalI and blunt-ended by using DNA Ligation kit (produced by Takara Shuzo).

A DNA in a ligation solution was introduced into Brevibacterium lactofermentum ATCC 13869 in accordance with an electric pulse method (Sugimoto et al., Japanese Patent Application Laid-open No. 2-207791). Transformants were selected on a complete medium containing 5 µg/ml of chloramphenicol. Plasmid DNA was collected from the transformants, and digested with EcoRI to obtain a plasmid in which the lysC promoter was ligated with the ppc structural gene in normal orientation. The obtained plasmid was designated as pAKPFds. The process of construction of pAKPFds is shown in Fig. 4. The ppc ligated with the lysC promoter is hereinafter referred to as "wild type high expression ppc".

(3) Insertion of wild type high expression ppc into vector

The wild type high expression ppc obtained in the above was amplified by PCR to insert it into a vector having a replication origin autonomously replicable in coryneform bacteria other than Brevi.-ori. As for DNA primers, an oligonucleotide corresponding to the *lysC* promoter portion (SEQ ID NO: 7), which was synthesized on the basis of a sequence of *lysC* known for *Corynebacterium glutamicum* (see *Molecular Microbiology*, 5(5), 1197-1204 (1991); *Mol. Gen. Genet.*, 224, 317-324 (1990)), and an oligonucleotide corresponding to the *ppc* portion (SEQ ID NO: 8), which was synthesized on the basis of a sequence of *ppc* known for *Corynebacterium glutamicum* (see O'Regan, M. et al., *Gene*, 77, 237-251 (1989)). These primers were designed so that a fragment of about 3,150 bp containing the wild type high expression ppc could be amplified and a terminal of the amplified DNA fragment could be digested a restriction enzyme *KpnI*. Synthesis of DNA and PCR were performed in the same manner as described in Example 1.

A cloning vector for coryneform bacteria, pVK7, which was newly constructed, was used as a vector for introducing the wild type high expression ppc into coryneform bacteria. pVK7 was constructed by ligating pHSG299, a vector for *E. coli* (Km^r; Takeshita, S. et al., *Gene*, 61, 63-74 (1987)) with pAM330, a cryptic plasmid for *Brevibacterium lactofermentum* as described below. pHSG299 was digested with a restriction enzyme resulting one cleavage site, *Avall* (produced by Takara Shuzo), blunt-ended by using T4 DNA polymerase, and ligated with pAM330 having been digested with *HindIII* (produced by Takara Shuzo) and blunt-ended by using T4 DNA polymerase. Depending on orientation of the inserted pAM330 in pHSG299, the two obtained plasmids were designated as pVK6 and pVK7, and pVK7 was used for the following experiments. pVK7 is autonomously replicable in both of *E. coli* and *Brevibacterium lactofermentum* and has a multiple cloning site originating from pHSG299 and *lacZ'*. The process of construction of pVK6 and pVK7 is shown in Fig. 5.

An amplified gene fragment of about 3,150 bp was confirmed by agarose gel electrophoresis, and then the fragment extracted from the gel was purified by an ordinary method and digested with a restriction enzyme *KpnI* (produced by Takara Shuzo). The DNA fragment was ligated with pVK7 having been digested with a restriction enzyme *KpnI*. The prepared plasmid was designated as pPwm. The process of construction of pPwm is shown in Fig. 6.

Example 4: Preparation of plasmid comprising combination of mutant *lysC* and *lysA*

A plasmid containing mutant *lysC*, *lysA*, and a replication origin for coryneform bacteria was prepared from plasmid p399AK9B containing mutant *lysC* and Brevi.-ori and plasmid p299LYSA containing *lysA*. p299LYSA was digested with restriction enzymes *BamHI* and *KpnI* (both produced by Takara Shuzo) and blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method. The obtained DNA fragment was ligated with p399AK9B having been digested with *Sall* and blunt-ended. Thus, a plasmid containing mutant *lysC* and *lysA* autonomously replicable in coryneform bacteria was prepared, and designated as pCL. The process of construction of pCL is shown in Fig. 7.

Comparative Example 1: Preparation of *dapA*, *dapB* and *ddh* from *Brevibacterium lactofermentum*

As genes associated with L-lysine biosynthesis other than *lysC*, *lysA* and *ppc*, *dapA* (dihydrodipicolinate synthase gene), *dapB* (dihydrodipicolinate reductase gene) and *ddh* (diaminopimelate dehydrogenase gene) were obtained as follows.

(1) Preparation of *dapA* and construction of plasmid containing *dapA*

A wild type strain of *Brevibacterium lactofermentum* ATCC 13869 was used as a chromosomal DNA donor. Chromosomal DNA was prepared from the ATCC 13869 strain in accordance with an ordinary method. A DNA fragment containing *dapA* was amplified from the chromosomal DNA in accordance with PCR. As for DNA primers used for amplification, DNA's of 20-mers having nucleotide sequences shown in SEQ ID NOs: 19 and 20 in Sequence Listing respectively were synthesized in order to amplify a region of about 1.5 kb coding for DDPS on the basis of a sequence known for *Corynebacterium glutamicum* (see *Nucleic Acids Research*, 18(21), 6421 (1990); *EMBL* accession No. X53993). Synthesis of DNA and PCR were performed in the same manner as described in Example 1. pCR1000 (produced by Invitrogen, see *Bio/Technology*, 9, 657-663 (1991)) was used as a cloning vector for the amplified gene fragment of 1,411 bp, and was ligated with the amplified *dapA* fragment. Ligation of DNA was performed by using DNA ligation kit (produced by Takara Shuzo) in accordance with a designated method. Thus a plasmid was constructed, in which the *dapA* fragment of 1,411 bp amplified from chromosome of *Brevibacterium lactofermentum* was ligated with pCR1000. The plasmid obtained as described above, which had *dapA* originating from ATCC 13869, was designated as pCRDAPA.

A transformant strain AJ13106 obtained by introducing pCRDAPA into *E. coli* JM109 strain has been internationally

deposited since May 26, 1995 under an accession number of FERM BP-5113 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology of Ministry of International Trade and Industry (1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, 305 Japan) based on the Budapest Treaty.

Brevi.-ori was introduced into the prepared pCRDAPA to construct a plasmid carrying dapA autonomously replicable in coryneform bacteria. pHK4 was digested with restriction enzymes KpnI and BamHI (produced by Takara Shuzo), and cleaved edges were blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method. After the blunt end formation, a phosphorylated SmaI linker (produced by Takara Shuzo) was ligated to make modification so that the DNA fragment corresponding to the Brevi.-ori portion might be excised from pHK4 by digestion with only SmaI. This plasmid was digested with SmaI, and the generated Brevi.-ori DNA fragment was ligated with pCRDAPA having been also digested with SmaI to prepare a plasmid containing dapA autonomously replicable in coryneform bacteria. This plasmid was designated as pDPSB. The process of construction of pDPSB(Km^r) is shown in Fig. 8.

(2) Preparation of dapB and construction of plasmid containing dapB

A wild type strain of Brevibacterium lactofermentum ATCC 13869 was used as a chromosomal DNA donor. Chromosomal DNA was prepared from the ATCC 13869 strain in accordance with an ordinary method. A DNA fragment containing dapB was amplified from the chromosomal DNA in accordance with PCR. As for DNA primers used for amplification, DNA's of 23-mers having nucleotide sequences depicted in SEQ ID NOs: 21 and 22 in Sequence Listing respectively were synthesized in order to amplify a region of about 2.0 kb coding for DDPR on the basis of a sequence known for Brevibacterium lactofermentum (see Journal of Bacteriology, 175(9), 2743-2749 (1993)). Synthesis of DNA and PCR were performed in the same manner as described in Example 1. pCR-Script (produced by Invitrogen) was used as a cloning vector for the amplified gene fragment of 2,001 bp, and was ligated with the amplified dapB fragment. Thus a plasmid was constructed, in which the dapB fragment of 2,001 bp amplified from chromosome of Brevibacterium lactofermentum was ligated with pCR-Script. The plasmid obtained as described above, which had dapB originating from ATCC 13869, was designated as pCRDAPB. A transformant strain AJ13107 obtained by introducing pCRDAPB into E. coli JM109 strain has been internationally deposited since May 26, 1995 under an accession number of FERM BP-5114 in National Institute of Bioscience and Human Technology of Agency of Industrial Science and Technology of Ministry of International Trade and Industry (1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, 305 Japan) based on the Budapest Treaty.

A fragment of 1,101 bp containing a structural gene of DDPR was extracted by digesting pCRDAPB with EcoRV and SphI. This fragment was ligated with pHSG399 having been digested with HincII and SphI to prepare a plasmid. The prepared plasmid was designated as p399DPR.

Brevi.-ori was introduced into the prepared p399DPR to construct a plasmid carrying dapB autonomously replicable in coryneform bacteria. pHK4 was digested with a restriction enzyme KpnI (produced by Takara Shuzo), and cleaved edges were blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method. After the blunt end formation, a phosphorylated BamHI linker (produced by Takara Shuzo) was ligated to make modification so that the DNA fragment corresponding to the Brevi.-ori portion might be excised from pHK4 by digestion with only BamHI. This plasmid was digested with BamHI, and the generated Brevi.-ori DNA fragment was ligated with p399DPR having been also digested with BamHI to prepare a plasmid containing dapB autonomously replicable in coryneform bacteria. The prepared plasmid was designated as pDPRB. The process of construction of pDPRB is shown in Fig. 9.

(3) Preparation of ddh and construction of plasmid containing ddh

A ddh gene was obtained by amplifying the ddh gene from chromosomal DNA of Brevibacterium lactofermentum ATCC 13869 in accordance with the PCR method by using two oligonucleotide primers (SEQ ID NOs: 23, 24) prepared on the basis of a known nucleotide sequence of a ddh gene of Corynebacterium glutamicum (Ishino, S. et al., Nucleic Acids Res., 15, 3917 (1987)). An obtained amplified DNA fragment was digested with EcoT22I and AvaI, and cleaved edges were blunt-ended. After that, the fragment was inserted into a SmaI site of pMW119 to obtain a plasmid pDDH.

Next, pDDH was digested with Sall and EcoRI, followed by blunt end formation. After that, an obtained fragment was ligated with pUC18 having been digested with SmaI. A plasmid thus obtained was designated as pUC18DDH.

Brevi.-ori was introduced into pUC18DDH to construct a plasmid carrying ddh autonomously replicable in coryneform bacteria. pHK4 was digested with restriction enzymes KpnI and BamHI, and cleaved edges were blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method. After the blunt end formation, a phosphorylated PstI linker (produced by Takara Shuzo) was ligated so that it was inserted into a PstI site of pHSG299. A plasmid constructed as described above was designated as pPK4. Next, pUC18DDH was digested with XbaI and KpnI, and a generated fragment was ligated with pPK4 having been

digested with KpnI and XbaI. Thus a plasmid containing ddh autonomously replicable in coryneform bacteria was constructed. This plasmid was designated as pPK4D. The process of construction of pPK4D is shown in Fig. 10.

Comparative Example 2: Construction of Plasmid Comprising Combination of Mutant lysC, and dapA, dapB or ddh

(1) Construction of combination of mutant lysC and dapA

A plasmid comprising mutant lysC, dapA, and replication origin of coryneform bacteria was constructed from the plasmid pCRDAPA comprising dapA and the plasmid p399AK9B comprising mutant lysC and Brevi.-ori. p399AK9B was completely digested with Sall, and then it was blunt-ended. An EcoRI linker was ligated thereto to construct a plasmid in which the Sall site was modified into an EcoRI site. The obtained plasmid was designated as p399AK9BSE. The mutant lysC and Brevi.-ori were excised as one fragment by partially digesting p399AK9BSE with EcoRI. This fragment was ligated with pCRDAPA having been digested with EcoRI. An obtained plasmid was designated as pCRCAB. This plasmid is autonomously replicable in E. coli and coryneform bacteria, and it gives kanamycin resistance to a host, the plasmid comprising a combination of mutant lysC and dapA. The process of construction of pCRCAB is shown in Fig. 11.

(2) Construction of Plasmid Comprising Combination of Mutant lysC and dapB

A plasmid comprising mutant lysC and dapB was constructed from the plasmid p399AK9 having mutant lysC and the plasmid p399DPR having dapB. A fragment of 1,101 bp containing a structural gene of DDR was extracted by digesting p399DPR with EcoRV and SphI. This fragment was ligated with p399AK9 having been digested with Sall and then blunt-ended and having been further digested with SphI to construct a plasmid comprising a combination of mutant lysC and dapB. This plasmid was designated as p399AKDDPR.

Next, Brevi.-ori was introduced into the obtained p399AKDDPR. The plasmid pHK4 containing Brevi.-ori was digested with a restriction enzyme KpnI (produced by Takara Shuzo), and cleaved edges were blunt-ended. Blunt end formation was performed by using DNA Blunting kit (produced by Takara Shuzo) in accordance with a designated method. After the blunt end formation, a phosphorylated BamHI linker (produced by Takara Shuzo) was ligated to make modification so that the DNA fragment corresponding to the Brevi.-ori portion might be excised from pHK4 by digestion with only BamHI. This plasmid was digested with BamHI, and the generated Brevi.-ori DNA fragment was ligated with p399AKDDPR having been also digested with BamHI to construct a plasmid containing mutant lysC and dapB autonomously replicable in coryneform bacteria. The constructed plasmid was designated as pCB. The process of construction of pCB is shown in Fig. 12.

(3) Construction of Plasmid Comprising Combination of mutant lysC and ddh

A plasmid containing mutant lysC, ddh, and a replication origin for coryneform bacteria was prepared from plasmid pUC18DDH containing ddh and plasmid p399AK9B containing mutant lysC and Brevi.-ori. pUC18DDH was digested with a restriction enzyme EcoRI (produced by Takara Shuzo), blunt-ended and ligated with a Sall polylinker at a terminal thereof to change EcoRI site to Sall site. The obtained plasmid was digested with Sall to obtain a DNA fragment containing ddh.

Then, p399AK9B was digested with a restriction enzyme Sall and ligated with the DNA fragment containing ddh. Thus, a plasmid containing mutant lysC, ddh and Brevi.-ori autonomously replicable in coryneform bacteria was prepared, and designated as pCD. The process of construction of pCD is shown in Fig. 13.

Example 5: Introduction of Plasmids Comprising Genes for L-Lysine Biosynthesis into L-Lysine-Producing Bacterium of Brevibacterium lactofermentum

The plasmids comprising the genes for L-lysine biosynthesis constructed as described above, namely p399AK9B(Cm^r), pLYSAB(Cm^r), pPwm(Km^r), pCRCAB(Km^r), pCB(Cm^r), pCD(Cm^r), and pCL(Cm^r) were introduced into an L-lysine-producing bacterium AJ11082 (NRRL B-11470) of Brevibacterium lactofermentum respectively. AJ11082 strain has a property of AEC resistance. The plasmids were introduced in accordance with an electric pulse method (Sugimoto et al., Japanese Patent Application Laid-open No. 2-207791). Transformants were selected based on drug resistance markers possessed by the respective plasmids. Transformants were selected on a complete medium containing 5 µg/ml of chloramphenicol when a plasmid comprising a chloramphenicol resistance gene was introduced, or transformants were selected on a complete medium containing 25 µg/ml of kanamycin when a plasmid comprising a kanamycin resistance gene was introduced.

To a strain which mutant lysC and lysA were enhanced among the obtained transformants, pPwm (Km^r) was intro-

duced to obtain a strain in which three of mutant lysC, lysA and ppc were enhanced (AJ11082/pCL/pPwm). Transformants were selected on a complete medium containing 5 µg/ml of chloramphenicol and 25 µg/ml of kanamycin.

Example 6: Production of L-Lysine

Each of the transformants obtained in Example 5 was cultivated in an L-lysine-producing medium to evaluate its L-lysine productivity. The L-lysine-producing medium had the following composition.

[L-Lysine-producing medium]

The following components other than calcium carbonate (in 1 L) were dissolved, and pH was adjusted at 8.0 with KOH. The medium was sterilized at 115°C for 15 minutes, and calcium carbonate (50 g) having been separately sterilized in hot air in a dry state was thereafter added thereto.

Glucose	100 g
(NH ₄) ₂ SO ₄	55 g
KH ₂ PO ₄	1 g
MgSO ₄ · 7H ₂ O	1 g
Biotin	500 µg
Thiamin	2000 µg
FeSO ₄ · 7H ₂ O	0.01 g
MnSO ₄ · 7H ₂ O	0.01 g
Nicotinamide	5 mg
Protein hydrolysate (Mamenou)	30 ml
Calcium carbonate	50 g

Each of the various types of the transformants and the parent strain was inoculated to the medium having the composition described above to perform cultivation at 31.5°C with reciprocating shaking. The amount of produced L-lysine after 40 or 72 hours of cultivation are shown in Table 1. In the table, lysC^{*} represents mutant lysC.

Table 1

Accumulation of L-Lysine after Cultivation for 40 or 72 Hours			
Bacterial strain/plasmid	Introduced gene	Amount of produced L-lysine(g/L)	
		after 40 hrs	after 72 hrs
AJ11082		22.0	29.8
AJ11082/p399AK9B	<u>lysC</u> [*]	16.8	34.5
AJ11082/pLYSAB	<u>lysA</u>	19.8	32.5
AJ11082/pPwm	<u>ppc</u>	20.7	28.9
AJ11082/pCRCAB	<u>lysC</u> [*] , <u>dapA</u>	19.7	36.5
AJ11082/pCB	<u>lysC</u> [*] , <u>dapB</u>	23.3	35.0
AJ11082/pCD	<u>lysC</u> [*] , <u>ddh</u>	15.0	27.0
AJ11082/pCL	<u>lysC</u> [*] , <u>lysA</u>	24.0	44.0
AJ11082/pCL/pPwm	<u>lysC</u> [*] , <u>lysA</u> , <u>ppc</u>	25.0	45.2

As shown in above, when mutant lysC, lysA, or ppc was enhanced singly, or when mutant lysC was enhanced in combination with dapA or ddh, the amount of produced L-lysine was larger than or equivalent to that produced by the parent strain after 72 hours of cultivation, however, the amount of produced L-lysine was smaller than that produced by the parent strain after 40 hours of cultivation. Namely, the L-lysine-producing speed was lowered in cultivation for a short period. Similarly, when mutant lysC and ddh were enhanced in combination, the amount of produced L-lysine was smaller than that produced by the parent strain after 40 hours and 72 hours of cultivation. On the contrary, in the case of the strain in which dapB was enhanced together with mutant lysC, the growth was improved, the L-lysine-producing speed was successfully restored in the short period of cultivation, and the accumulated amount of L-lysine was also improved in the long period of cultivation. In the case of the strain in which three of mutant lysC, lysA, and ppc were simultaneously enhanced, the L-lysine productivity was further improved.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: AJINOMOTO CO., LTD.
- (ii) TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE:
 - (B) STREET:
 - (C) CITY:
 - (E) COUNTRY:
 - (F) ZIP:
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 8-325658
 - (B) FILING DATE: 05-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME:
 - (B) REGISTRATION NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE:
 - (B) TELEFAX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iv) ANTI-SENSE: no
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
TCGCGAAGTA GCACCTGTCA CTT

23

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (iv) ANTI-SENSE: yes
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
ACGGAATTCA ATCTTACGGC C

21

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1643 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Brevibacterium lactofermentum*
 (B) STRAIN: ATCC 13869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

10	TCGCGAAGTA	GCACCTGTCA	CTTTGTCTC	AAATATTAA	TCGAATATCA	ATATACGGTC	60
	TGTTTATTGG	AACGCATCCC	AGTGGCTGAG	ACGCATCCGC	TAAAGCCCCA	GGAACCCTGT	120
	GCAGAAAGAA	AACACTCCTC	TGGCTAGGTA	GACACAGTTT	ATAAAGGTAG	AGTTGAGCGG	180
	GTAAGTGTCA	GCACGTAGAT	CGAAAGGTGC	ACAAAGGTGG	CCCTGGTCGT	ACAGAAATAT	240
	GGCGGTTTCT	CGCTTGAGAG	TGCGGAACGC	ATTAGAAACG	TCGCTGAACG	GATCGTTGCC	300
	ACCAAGAAGG	CTGGAATGA	TGTCGTGGTT	GTCTGCTCCG	CAATGGGAGA	CACCACGGAT	360
15	GAACTTCTAG	AACTTGCAGC	GGCAGTGAAT	CCC GTTCCGC	CAGCTCGTGA	AATGGATATG	420
	CTCCTGACTG	CTGGTGAGCG	TATTTCTAAC	GCTCTCGTCG	CCATGGCTAT	TGAGTCCCTT	480
	GGCGCAGAAG	CTCAATCTTT	CACTGGCTCT	CAGGCTGGTG	TGCTCACCAC	CGAGCGCCAC	540
	GGAAACGCAC	GCATTGTTGA	CGTCACACCG	GGTCGTGTGC	GTGAAGCACT	CGATGAGGGC	600
	AAGATCTGCA	TTGTTGCTGG	TTTTCAGGGT	GTTAATAAAG	AAACCCQCGA	TGTCACCACG	660
20	TTGGGTCGTG	GTGGTTCTGA	CACCACTGCA	GTTGCGTTGG	CAGCTGCTTT	GAACGCTGAT	720
	GTGTGTGAGA	TTTACTCGGA	CGTTGACGGT	GTGTATACCG	CTGACCCGCG	CATCGTTTCT	780
	AATGCACAGA	AGCTGGAATA	GCTCAGCTTC	GAAGAAATGC	TGGAACCTGC	TGCTGTTGGC	840
	TCCAAGATTT	TGGTGCTGCG	CAGTGTGAA	TACGCTCGTG	CATTCAATGT	GCCACTTCGC	900
	GTACGCTCGT	CTTATAGTAA	TGATCCCGGC	ACTTTGATTG	CCGGCTCTAT	GGAGGATATT	960
	CCTGTGGAAG	AAGCAGTCCT	TACCGGTGTC	GCAACCGACA	AGTCCGAAGC	CAAAGTAACC	1020
25	GTTCTGGGTA	TTTCCGATAA	GCCAGGCGAG	GCTGCCAAGG	TTTCCGTGTC	GTTGGCTGAT	1080
	GCAGAAATCA	ACATTGACAT	GGTCTGTCAG	AACGTCTCCT	CTGTGGAAGA	CGGCACCACC	1140
	GACATCACGT	TCACCTGCCC	TCGCGCTGAC	GGACGCCGTG	CGATGGAGAT	CTTGAAGAAG	1200
	CTTCAGGTTC	AGGGCAACTG	GACCAATGTG	CTTTACGACG	ACCAGGTCGG	CAAAGTCTCC	1260
	CTCGTGGGTG	CTGGCATGAA	GTCTCACCCA	GGTGTTACCG	CAGAGTTCAT	GGAGGCTCTG	1320
	CGCGATGTCA	ACGTGAACAT	CGAATTGATT	TCCACCTCTG	AGATCCGCAT	TTCCGTGCTG	1380
30	ATCCGTGAAG	ATGATCTGGA	TGCTGCTGCA	CGTGCAATTG	ATGAGCAGTT	CCAGCTGGGC	1440
	GGCGAAGACG	AAGCCGTCGT	TTATGCAGGC	ACCGGACGCT	AAAGTTTTAA	AGGAGTAGTT	1500
	TTACAATGAC	CACCATCGCA	GTTGTTGGTG	CAACCGGCCA	GGTCGGCCAG	GTTATGCGCA	1560
	CCCTTTTGGA	AGAGCGCAAT	TTCCCAGCTG	ACACTGTTCT	TTTCTTTGCT	TCCCCGCGTT	1620
	CCGCAGGCCG	TAAGATTGAA	TTC				1643

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1643 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevibacterium lactofermentum*
 (B) STRAIN: ATCC 13869

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 217..1482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

50	TCGCGAAGTA	GCACCTGTCA	CTTTGTCTC	AAATATTAA	TCGAATATCA	ATATACGGTC	60
	TGTTTATTGG	AACGCATCCC	AGTGGCTGAG	ACGCATCCGC	TAAAGCCCCA	GGAACCCTGT	120
	GCAGAAAGAA	AACACTCCTC	TGGCTAGGTA	GACACAGTTT	ATAAAGGTAG	AGTTGAGCGG	180
	GTAAGTGTCA	GCACGTAGAT	CGAAAGGTGC	ACAAAG GTG	GCC CTG GTC GTA CAG		234

Met Ala Leu Val Val Gln

1

5

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	AAA	TAT	GGC	GGT	TCC	TCG	CTT	GAG	AGT	GCG	GAA	CGC	ATT	AGA	AAC	GTC	282
	Lys	Tyr	Gly	Gly	Ser	Ser	Leu	Glu	Ser	Ala	Glu	Arg	Ile	Arg	Asn	Val	
			10						15					20			
5	GCT	GAA	CGG	ATC	GTT	GCC	ACC	AAG	AAG	GCT	GGA	AAT	GAT	GTC	GTG	GTT	330
	Ala	Glu	Arg	Ile	Val	Ala	Thr	Lys	Lys	Ala	Gly	Asn	Asp	Val	Val	Val	
			25					30					35				
	GTC	TGC	TCC	GCA	ATG	GGA	GAC	ACC	ACG	GAT	GAA	CTT	CTA	GAA	CTT	GCA	378
	Val	Cys	Ser	Ala	Met	Gly	Asp	Thr	Thr	Asp	Glu	Leu	Leu	Glu	Leu	Ala	
			40				45					50					
10	GCG	GCA	GTG	AAT	CCC	GTT	CCG	CCA	GCT	CGT	GAA	ATG	GAT	ATG	CTC	CTG	426
	Ala	Ala	Val	Asn	Pro	Val	Pro	Pro	Ala	Arg	Glu	Met	Asp	Met	Leu	Leu	
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	ACT	GCT	GGT	GAG	CGT	ATT	TCT	AAC	GCT	CTC	GTC	GCC	ATG	GCT	ATT	GAG	474
	Thr	Ala	Gly	Glu	Arg	Ile	Ser	Asn	Ala	Leu	Val	Ala	Met	Ala	Ile	Glu	
				75					80					85			
15	TCC	CTT	GGC	GCA	GAA	GCT	CAA	TCT	TTC	ACT	GGC	TCT	CAG	GCT	GGT	GTG	522
	Ser	Leu	Gly	Ala	Glu	Ala	Gln	Ser	Phe	Thr	Gly	Ser	Gln	Ala	Gly	Val	
			90					95					100				
	CTC	ACC	ACC	GAG	CGC	CAC	GGA	AAC	GCA	CGC	ATT	GTT	GAC	GTC	ACA	CCG	570
	Leu	Thr	Thr	Glu	Arg	His	Gly	Asn	Ala	Arg	Ile	Val	Asp	Val	Thr	Pro	
			105					110					115				
20	GGT	CGT	GTG	CGT	GAA	GCA	CTC	GAT	GAG	GGC	AAG	ATC	TGC	ATT	GTT	GCT	618
	Gly	Arg	Val	Arg	Glu	Ala	Leu	Asp	Glu	Gly	Lys	Ile	Cys	Ile	Val	Ala	
			120				125				130						
	GGT	TTT	CAG	GGT	GTT	AAT	AAA	GAA	ACC	CGC	GAT	GTC	ACC	ACG	TTG	GGT	666
	Gly	Phe	Gln	Gly	Val	Asn	Lys	Glu	Thr	Arg	Asp	Val	Thr	Thr	Leu	Gly	
			135			140					145				150		
25	CGT	GGT	GGT	TCT	GAC	ACC	ACT	GCA	GTT	GCG	TTG	GCA	GCT	GCT	TTG	AAC	714
	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala	Leu	Ala	Ala	Ala	Leu	Asn	
				155				160					165				
	GCT	GAT	GTG	TGT	GAG	ATT	TAC	TCG	GAC	GTT	GAC	GGT	GTG	TAT	ACC	GCT	762
	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val	Asp	Gly	Val	Tyr	Thr	Ala	
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	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys	Leu	Glu	Lys	Leu	Ser	Phe	
			185				190						195				
	GAA	GAA	ATG	CTG	GAA	CTT	GCT	GTT	GGC	TCC	AAG	ATT	TTG	GTG	CTG		858
	Glu	Glu	Met	Leu	Glu	Leu	Ala	Val	Gly	Ser	Lys	Ile	Leu	Val	Leu		
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	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn	Val	Pro	Leu	Arg	Val	Arg	
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40	TCG	TCT	TAT	AGT	AAT	GAT	CCC	GGC	ACT	TTG	ATT	GCC	GGC	TCT	ATG	GAG	954
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	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr	Gly	Val	Ala	Thr	Asp	Lys	
				250				255					260				
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	GCT	GCC	AAG	GTT	TTC	CGT	GCG	TTG	GCT	GAT	GCA	GAA	ATC	AAC	ATT	GAC	1098
	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp	Ala	Glu	Ile	Asn	Ile	Asp	
			280				285					290					
50	ATG	GTT	CTG	CAG	AAC	GTC	TCC	TCT	GTG	GAA	GAC	GGC	ACC	ACC	GAC	ATC	1146
	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu	Asp	Gly	Thr	Thr	Asp	Ile	
			295			300					305					310	

55

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ACG TTC ACC TGC CCT CGC GCT GAC GGA CGC CGT GCG ATG GAG ATC TTG 1194
 Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg Arg Ala Met Glu Ile Leu
 315 320 325
 5 AAG AAG CTT CAG GTT CAG GGC AAC TGG ACC AAT GTG CTT TAC GAC GAC 1242
 Lys Lys Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp Asp
 330 335 340
 CAG GTC GGC AAA GTC TCC CTC GTG GGT GCT GGC ATG AAG TCT CAC CCA 1290
 Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His Pro
 345 350 355
 10 GGT GTT ACC GCA GAG TTC ATG GAA GCT CTG CGC GAT GTC AAC GTG AAC 1338
 Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val Asn
 360 365 370
 ATC GAA TTG ATT TCC ACC TCT GAG ATC CGC ATT TCC GTG CTG ATC CGT 1386
 Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile Arg
 375 380 385 390
 15 GAA GAT GAT CTG GAT GCT GCT GCA CGT GCA TTG CAT GAG CAG TTC CAG 1434
 Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe Gln
 395 400 405
 CTG GGC GGC GAA GAC GAA GCC GTC GTT TAT GCA GGC ACC GGA CGC TAA 1482
 Leu Gly Gly Glu Asp Glu Ala Val Tyr Ala Gly Thr Gly Arg
 410 415 420
 20 AGTTTAAAG GAGTAGTTT ACAATGACCA CCATCGCAGT TGTTGGTGCA ACCGGCCAGG 1542
 TCGGCCAGGT TATGCGCACC CTTTGGGAAG AGCGCAATTT CCCAGCTGAC ACTGTTCTGTT 1602
 TCTTTGCTTC CCCGCGTTC GCAGGCCGTA AGATTGAATT C 1643

(2) INFORMATION FOR SEQ ID NO:5:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 30 Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
 1 5 10 15
 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 35 40 45
 Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 40 85 90 95
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125
 45 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160
 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175
 50 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205

55

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
 305 310 315 320
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415
 Ala Gly Thr Gly Arg
 420

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1643 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Brevibacterium lactofermentum
 (B) STRAIN: ATCC 13869

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 964..1482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCGCGAAGTA	GCACCTGTCA	CTTTTGTCTC	AAATATTAAA	TCGAATATCA	ATATACGGTC	60
TGTTTATTGG	AACGCATCCC	AGTGGCTGAG	ACGCATCCGC	TAAAGCCCCA	GGAACCCTGT	120
GCAGAAAGAA	AACACTCCTC	TGGCTAGGTA	GACACAGTTT	ATAAAGGTAG	AGTTGAGCGG	180
GTAACGTGCA	GCACGTAGAT	CGAAAGGTGC	ACAAAGGTGG	CCCTGGTCGT	ACAGAAATAT	240
GGCGGTTTCT	CGCTTGAGAG	TGCGGAACGC	ATTAGAAACG	TCGCTGAACG	GATCGTTGCC	300
ACCAAGAAGG	CTGGAAATGA	TGTCGTGGTT	GTCTGCTCCG	CAATGGGAGA	CACCACGGAT	360
GAACCTCTAG	AACTTGCAGC	GGCAGTGAAT	CCCGTTCCGC	CAGCTCGTGA	AATGGATATG	420
CTCCTGACTG	CTGGTGAGCG	TATTTCTAAC	GCTCTCGTCG	CCATGGCTAT	TGAGTCCCTT	480
GGCGCAGAAG	CTCAATCTTT	CACTGGCTCT	CAGGCTGGTG	TGCTCACCAC	CGAGCGCCAC	540
GGAAACGCAC	GCATTGTTGA	CGTCACACCG	GGTCGTGTGC	GTGAAGCACT	CGATGAGGGC	600
AAGATCTGCA	TTGTTGCTGG	TTTTCAGGGT	GTTAATAAAG	AAACCCGCGA	TGTCACCACG	660
TTGGGTCGTG	GTGGTTCTGA	CACCACTGCA	GTTGCGTTGG	CAGCTGCTTT	GAACGCTGAT	720
GTGTGTGAGA	TTTACTCGGA	CGTTGACGGT	GTGTATACCG	CTGACCCGCG	CATCGTTTCT	780
AATGCACAGA	AGCTGGAAAA	GCTCAGCTTC	GAAGAAATGC	TGGAACCTGC	TGCTGTTGGC	840
TCCAAGATTT	TGGTGCTGCG	CAGTGTGAA	TACGCTCGTG	CATTCAATGT	GCCACTTCGC	900

GTACGCTCGT CTTATAGTAA TGATCCCGGC ACTTTGATTG CCGGCTCTAT GGAGGATATT 960
 CCT GTG GAA GAA GCA GTC CTT ACC GGT GTC GCA ACC GAC AAG TCC GAA 1008
 Met Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp Lys Ser Glu
 1 5 10 15
 GCC AAA GTA ACC GTT CTG GGT ATT TCC GAT AAG CCA GGC GAG GCT GCC 1056
 Ala Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly Glu Ala Ala
 20 25 30
 AAG GTT TTC CGT GCG TTG GCT GAT GCA GAA ATC AAC ATT GAC ATG GTT 1104
 Lys Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile Asp Met Val
 35 40 45
 CTG CAG AAC GTC TCC TCT GTG GAA GAC GGC ACC ACC GAC ATC ACG TTC 1152
 Leu Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp Ile Thr Phe
 50 55 60
 ACC TGC CCT CGC GCT GAC GGA CGC CGT GCG ATG GAG ATC TTG AAG AAG 1200
 Thr Cys Pro Arg Ala Asp Gly Arg Arg Ala Met Glu Ile Leu Lys Lys
 65 70 75
 CTT CAG GTT CAG GGC AAC TGG ACC AAT GTG CTT TAC GAC GAC CAG GTC 1248
 Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp Asp Gln Val
 80 85 90 95
 GGC AAA GTC TCC CTC GTG GGT GCT GGC ATG AAG TCT CAC CCA GGT GTT 1296
 Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His Pro Gly Val
 100 105 110
 ACC GCA GAG TTC ATG GAA GCT CTG CGC GAT GTC AAC GTG AAC ATC GAA 1344
 Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val Asn Ile Glu
 115 120 125
 TTG ATT TCC ACC TCT GAG ATC CGC ATT TCC GTG CTG ATC CGT GAA GAT 1392
 Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile Arg Glu Asp
 130 135 140
 GAT CTG GAT GCT GCT GCA CGT GCA TTG CAT GAG CAG TTC CAG CTG GGC 1440
 Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe Gln Leu Gly
 145 150 155
 GGC GAA GAC GAA GCC GTC GTT TAT GCA GGC ACC GGA CGC TAAAGTTTAA 1490
 Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
 160 165 170
 AGGAGTAGTT TTACAATGAC CACCATCGCA GTTGTTGGTG CAACCGGCCA GGTCGGCCAG 1550
 GTTATGCGCA CCCTTTTGGG AGAGCGCAAT TTCCCAGCTG ACACTGTTCTG TTTCTTTGCT 1610
 TCCCCGCGTT CCGCAGGCCG TAAGATTGAA TTC 1643

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp Lys Ser Glu Ala
 1 5 10 15
 Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly Glu Ala Ala Lys
 20 25 30
 Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile Asp Met Val Leu
 35 40 45
 Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp Ile Thr Phe Thr
 50 55 60
 Cys Pro Arg Ala Asp Gly Arg Arg Ala Met Glu Ile Leu Lys Lys Leu
 65 70 75 80
 Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp Asp Gln Val Gly
 85 90 95

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Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His Pro Gly Val Thr
100 105 110
Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val Asn Ile Glu Leu
115 120 125
Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile Arg Glu Asp Asp
130 135 140
Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe Gln Leu Gly Gly
145 150 155 160
Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
165 170

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTGGAGCCGA CCATTCCGCG AGG

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCAAAACCGC CCTCCACGGC GAA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3579 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Brevibacterium lactofermentum

(B) STRAIN: ATCC 13869

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 533..2182

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2188..3522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTGGAGCCGA CCATTCCGCG AGGCTGCACT GCAACGAGGT CGTAGTTTTG GTACATGGCT 60
TCTGGCCAGT TCATGGATTG GCTGCCGAAG AAGCTATAGG CATCGCACCA GGGCCACCGA 120
GTTACCGAAG ATGGTGCCGT GCTTTTCGCC TTGGGCAGGG ACCTTGACAA AGCCCACGCT 180
GATATCGCCA AGTGAGGGAT CAGAATAGTG CATGGGCACG TCGATGCTGC CACATTGAGC 240
GGAGGCAATA TCTACCTGAG GTGGGCATTC TTCCCAGCGG ATGTTTTCTT GCGCTGCTGC 300

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AGTGGGCATT GATACCAAAA AGGGGCTAAG CGCAGTCGAG GCGGCAAGAA CTGCTACTAC 360
 CCTTTTATT GTCGAACGGG GCATTACGGC TCCAAGGACG TTTGTTTCT GGGTCAGTTA 420
 CCCC AAAAAG CATATACAGA GACCAATGAT TTTTCATTAA AAAGGCAGGG ATTTGTTATA 480
 5 AGTATGGGTC GTATTCTGTG CGACGGGTGT ACCTCGGCTA GAATTTCTCC CC ATG 535
 Met
 1
 ACA CCA GCT GAT CTC GCA ACA TTG ATT AAA GAG ACC GCG GTA GAG GTT 583
 Thr Pro Ala Asp Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu Val
 5 10 15
 10 TTG ACC TCC CGC GAG CTC GAT ACT TCT GTT CTT CCG GAG CAG GTA GTT 631
 Leu Thr Ser Arg Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val Val
 20 25 30
 GTG GAG CGT CCG CGT AAC CCA GAG CAC GGC GAT TAC GCC ACC AAC ATT 679
 Val Glu Arg Pro Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn Ile
 35 40 45
 15 GCA TTG CAG GTG GCT AAA AAG GTC GGT CAG AAC CCT CGG GAT TTG GCT 727
 Ala Leu Gln Val Ala Lys Val Gly Gln Asn Pro Arg Asp Leu Ala
 50 55 60 65
 ACC TGG CTG GCA GAG GCA TTG GCT GCA GAT GAC GCC ATT GAT TCT GCT 775
 Thr Trp Leu Ala Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser Ala
 70 75 80
 20 GAA ATT GCT GGC CCA GGC TTT TTG AAC ATT CGC CTT GCT GCA GCA GCA 823
 Glu Ile Ala Gly Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala Ala
 85 90 95
 CAG GGT GAA ATT GTG GCC AAG ATT CTG GCA CAG GGC GAG ACT TTC GGA 871
 Gln Gly Glu Ile Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe Gly
 100 105 110
 25 AAC TCC GAT CAC CTT TCC CAC TTG GAC GTG AAC CTC GAG TTC GTT TCT 919
 Asn Ser Asp His Leu Ser His Leu Asp Val Asn Leu Glu Phe Val Ser
 115 120 125
 GCA AAC CCA ACC GGA CCT ATT CAC CTT GGC GGA ACC CGC TGG GCT GCC 967
 Ala Asn Pro Thr Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala Ala
 130 135 140 145
 GTG GGT GAC TCT TTG GGT CGT GTG CTG GAG GCT TCC GGC GCG AAA GTG 1015
 Val Gly Asp Ser Leu Gly Arg Val Leu Glu Ala Ser Gly Ala Lys Val
 150 155 160
 ACC CGC GAA TAC TAC TTC AAC GAT CAC GGT CGC CAG ATC GAT CGT TTC 1063
 Thr Arg Glu Tyr Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg Phe
 165 170 175
 GCT TTG TCC CTT CTT GCA GCG GCG AAG GGC GAG CCA ACG CCA GAA GAC 1111
 Ala Leu Ser Leu Leu Ala Ala Ala Lys Gly Glu Pro Thr Pro Glu Asp
 180 185 190
 40 GGT TAT GGC GGC GAA TAC ATT AAG GAA ATT GCG GAG GCA ATC GTC GAA 1159
 Gly Tyr Gly Gly Glu Tyr Ile Lys Glu Ile Ala Glu Ala Ile Val Glu
 195 200 205
 AAG CAT CCT GAA GCG TTG GCT TTG GAG CCT GCC GCA ACC CAG GAG CTT 1207
 Lys His Pro Glu Ala Leu Ala Leu Glu Pro Ala Thr Gln Glu Leu
 210 215 220 225
 45 TTC CGC GCT GAA GGC GTG GAG ATG ATG TTC GAG CAC ATC AAA TCT TCC 1255
 Phe Arg Ala Glu Gly Val Glu Met Met Phe Glu His Ile Lys Ser Ser
 230 235 240
 CTG CAT GAG TTC GGC ACC GAT TTC GAT GTC TAC TAC CAC GAG AAC TCC 1303
 Leu His Glu Phe Gly Thr Asp Phe Asp Val Tyr Tyr His Glu Asn Ser
 245 250 255
 50 CTG TTC GAG TCC GGT GCG GTG GAC AAG GCC GTG CAG GTG CTG AAG GAC 1351
 Leu Phe Glu Ser Gly Ala Val Asp Lys Ala Val Gln Val Leu Lys Asp
 260 265 270

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	AAC GGC AAC CTG TAC GAA AAC GAG GGC GCT TGG TGG CTG CGT TCC ACC	1399
	Asn Gly Asn Leu Tyr Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser Thr	
	275 280 285	
5	GAA TTC GGC GAT GAC AAA GAC CGC GTG GTG ATC AAG TCT GAC GGC GAC	1447
	Glu Phe Gly Asp Asp Lys Asp Arg Val Val Ile Lys Ser Asp Gly Asp	
	290 295 300 305	
	GCA GCC TAC ATC GCT GGC GAT ATC GCG TAC GTG GCT GAT AAG TTC TCC	1495
	Ala Ala Tyr Ile Ala Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe Ser	
	310 315 320	
10	CGC GGA CAC AAC CTA AAC ATC TAC ATG TTG GGT GCT GAC CAC CAT GGT	1543
	Arg Gly His Asn Leu Asn Ile Tyr Met Leu Gly Ala Asp His His Gly	
	325 330 335	
	TAC ATC GCG CGC CTG AAG GCA GCG GCG GCG GCA CTT GGC TAC AAG CCA	1591
	Tyr Ile Ala Arg Leu Lys Ala Ala Ala Ala Leu Gly Tyr Lys Pro	
	340 345 350	
15	GAA GGC GTT GAA GTC CTG ATT GGC CAG ATG GTG AAC CTG CTT CGC GAC	1639
	Glu Gly Val Glu Val Leu Ile Gly Gln Met Val Asn Leu Leu Arg Asp	
	355 360 365	
	GGC AAG GCA GTG CGT ATG TCC AAG CGT GCA GGC ACC GTG GTC ACC CTA	1687
	Gly Lys Ala Val Arg Met Ser Lys Arg Ala Gly Thr Val Val Thr Leu	
20	370 375 380 385	
	GAT GAC CTC GTT GAA GCA ATC GGC ATC GAT GCG GCG CGT TAC TCC CTG	1735
	Asp Asp Leu Val Glu Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser Leu	
	390 395 400	
	ATC CGT TCC TCC GTG GAT TCT TCC CTG GAT ATC GAT CTC GGC CTG TGG	1783
	Ile Arg Ser Ser Val Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu Trp	
25	405 410 415	
	GAA TCC CAG TCC TCC GAC AAC CCT GTG TAC TAC GTG CAG TAC GGA CAC	1831
	Glu Ser Gln Ser Ser Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly His	
	420 425 430	
	GCT CGT CTG TGC TCC ATC GCG CGC AAG GCA GAG ACC TTG GGT GTC ACC	1879
	Ala Arg Leu Cys Ser Ile Ala Arg Lys Ala Glu Thr Leu Gly Val Thr	
30	435 440 445	
	GAG GAA GGC GCA GAC CTA TCT CTA CTG ACC CAC GAC CGC GAA GGC GAT	1927
	Glu Glu Gly Ala Asp Leu Ser Leu Leu Thr His Asp Arg Glu Gly Asp	
	450 455 460 465	
	CTC ATC CGC ACA CTC GGA GAG TTC CCA GCA GTG GTG AAG GCT GCC GCT	1975
35	Leu Ile Arg Thr Leu Gly Glu Phe Pro Ala Val Val Lys Ala Ala Ala	
	470 475 480	
	GAC CTA CGT GAA CCA CAC CGC ATT GCC CGC TAT GCT GAG GAA TTA GCT	2023
	Asp Leu Arg Glu Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu Ala	
	485 490 495	
	GGA ACT TTC CAC CGC TTC TAC GAT TCC TGC CAC ATC CTT CCA AAG GTT	2071
40	Gly Thr Phe His Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys Val	
	500 505 510	
	GAT GAG GAT ACG GCA CCA ATC CAC ACA GCA CGT CTG GCA CTT GCA GCA	2119
	Asp Glu Asp Thr Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala Ala	
	515 520 525	
45	GCA ACC CGC CAG ACC CTC GCT AAC GCC CTG CAC CTG GTT GGC GTT TCC	2167
	Ala Thr Arg Gln Thr Leu Ala Asn Ala Leu His Leu Val Gly Val Ser	
	530 535 540 545	
	GCA CCG GAG AAG ATG TAACA ATG GCT ACA GTT GAA AAT TTC AAT GAA	2214
	Ala Pro Glu Lys Met Met Ala Thr Val Glu Asn Phe Asn Glu	
	550 1 5	
50	CTT CCC GCA CAC GTA TGG CCA CGC AAT GCC GTG CGC CAA GAA GAC GGC	2262
	Leu Pro Ala His Val Trp Pro Arg Asn Ala Val Arg Gln Glu Asp Gly	
	10 15 20 25	

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	GTT	GTC	ACC	GTC	GCT	GGT	GTG	CCT	CTG	CCT	GAC	CTC	GCT	GAA	GAA	TAC	2310
	Val	Val	Thr	Val	Ala	Gly	Val	Pro	Leu	Pro	Asp	Leu	Ala	Glu	Glu	Tyr	
				30						35				40			
5	GGA	ACC	CCA	CTG	TTC	GTA	GTC	GAC	GAG	GAC	GAT	TTC	CGT	TCC	CGC	TGT	2358
	Gly	Thr	Pro	Leu	Phe	Val	Val	Asp	Glu	Asp	Asp	Phe	Arg	Ser	Arg	Cys	
				45					50					55			
	CGC	GAC	ATG	GCT	ACC	GCA	TTC	GGT	GGA	CCA	GGC	AAT	GTG	CAC	TAC	GCA	2406
	Arg	Asp	Met	Ala	Thr	Ala	Phe	Gly	Gly	Pro	Gly	Asn	Val	His	Tyr	Ala	
			60					65				70					
10	TCT	AAA	GCG	TTC	CTG	ACC	AAG	ACC	ATT	GCA	CGT	TGG	GTT	GAT	GAA	GAG	2454
	Ser	Lys	Ala	Phe	Leu	Thr	Lys	Thr	Ile	Ala	Arg	Trp	Val	Asp	Glu	Glu	
		75					80					85					
	GGG	CTG	GCA	CTG	GAC	ATT	GCA	TCC	ATC	AAC	GAA	CTG	GGC	ATT	GCC	CTG	2502
	Gly	Leu	Ala	Leu	Asp	Ile	Ala	Ser	Ile	Asn	Glu	Leu	Gly	Ile	Ala	Leu	
		90				95				100				105			
15	GCC	GCT	GGT	TTC	CCC	GCC	AGC	CGT	ATC	ACC	GCG	CAC	GGC	AAC	AAC	AAA	2550
	Ala	Ala	Gly	Phe	Pro	Ala	Ser	Arg	Ile	Thr	Ala	His	Gly	Asn	Asn	Lys	
				110						115				120			
	GGC	GTA	GAG	TTC	CTG	CGC	GCG	TTG	GTT	CAA	AAC	GGT	GTG	GGA	CAC	GTG	2598
	Gly	Val	Glu	Phe	Leu	Arg	Ala	Leu	Val	Gln	Asn	Gly	Val	Gly	His	Val	
			125					130					135				
20	GTG	CTG	GAC	TCC	GCA	CAG	GAA	CTA	GAA	CTG	TTG	GAT	TAC	GTT	GCC	GCT	2646
	Val	Leu	Asp	Ser	Ala	Gln	Glu	Leu	Glu	Leu	Leu	Asp	Tyr	Val	Ala	Ala	
			140				145					150					
	GGT	GAA	GGC	AAG	ATT	CAG	GAC	GTG	TTG	ATC	CGC	GTA	AAG	CCA	GGC	ATC	2694
	Gly	Glu	Gly	Lys	Ile	Gln	Asp	Val	Leu	Ile	Arg	Val	Lys	Pro	Gly	Ile	
		155				160					165						
25	GAA	GCA	CAC	ACC	CAC	GAG	TTC	ATC	GCC	ACT	AGC	CAC	GAA	GAC	CAG	AAG	2742
	Glu	Ala	His	Thr	His	Glu	Phe	Ile	Ala	Thr	Ser	His	Glu	Asp	Gln	Lys	
		170			175					180					185		
	TTC	GGA	TTC	TCC	CTG	GCA	TCC	GGT	TCC	GCA	TTC	GAA	GCA	GCA	AAA	GCC	2790
	Phe	Gly	Phe	Ser	Leu	Ala	Ser	Gly	Ser	Ala	Phe	Glu	Ala	Ala	Lys	Ala	
				190					195					200			
30	GCC	AAC	AAC	GCA	GAA	AAC	CTG	AAC	CTG	GTT	GGC	CTG	CAC	TGC	CAC	GTT	2838
	Ala	Asn	Asn	Ala	Glu	Asn	Leu	Asn	Leu	Val	Gly	Leu	His	Cys	His	Val	
				205				210						215			
	GGT	TCC	CAG	GTG	TTC	GAC	GCC	GAA	GGC	TTC	AAG	CTG	GCA	GCA	GAA	CGC	2886
	Gly	Ser	Gln	Val	Phe	Asp	Ala	Glu	Gly	Phe	Lys	Leu	Ala	Ala	Glu	Arg	
			220				225					230					
	GTG	TTG	GGC	CTG	TAC	TCA	CAG	ATC	CAC	AGC	GAA	CTG	GGC	GTT	GCC	CTT	2934
	Val	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	His	Ser	Glu	Leu	Gly	Val	Ala	Leu	
		235				240					245						
40	CCT	GAA	CTG	GAT	CTC	GGT	GGC	GGA	TAC	GGC	ATT	GCC	TAT	ACC	GCA	GCT	2982
	Pro	Glu	Leu	Asp	Leu	Gly	Gly	Gly	Tyr	Gly	Ile	Ala	Tyr	Thr	Ala	Ala	
		250			255				260					265			
	GAA	GAA	CCA	CTC	AAC	GTC	GCA	GAA	GTT	GCC	TCC	GAC	CTG	CTC	ACC	GCA	3030
	Glu	Glu	Pro	Leu	Asn	Val	Ala	Glu	Val	Ala	Ser	Asp	Leu	Leu	Thr	Ala	
				270				275						280			
	GTC	GGA	AAA	ATG	GCA	GCG	GAA	CTA	GGC	ATC	GAC	GCA	CCA	ACC	GTG	CTT	3078
	Val	Gly	Lys	Met	Ala	Ala	Glu	Leu	Gly	Ile	Asp	Ala	Pro	Thr	Val	Leu	
			285					290						295			
	GTT	GAG	CCC	GGC	CGC	GCT	ATC	GCA	GGC	CCC	TCC	ACC	GTG	ACC	ATC	TAC	3126
	Val	Glu	Pro	Gly	Arg	Ala	Ile	Ala	Gly	Pro	Ser	Thr	Val	Thr	Ile	Tyr	
			300				305					310					
50	GAA	GTC	GGC	ACC	ACC	AAA	GAC	GTC	CAC	GTA	GAC	GAC	GAC	AAA	ACC	CGC	3174
	Glu	Val	Gly	Thr	Thr	Lys	Asp	Val	His	Val	Asp	Asp	Asp	Lys	Thr	Arg	
		315				320					325						

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CGT TAC ATC GCC GTG GAC GGA GGC ATG TCC GAC AAC ATC CGC CCA GCA 3222
 Arg Tyr Ile Ala Val Asp Gly Gly Met Ser Asp Asn Ile Arg Pro Ala 345
 330 335 340 345
 5 CTC TAC GGC TCC GAA TAC GAC GCC CGC GTA GTA TCC CGC TTC GCC GAA 3270
 Leu Tyr Gly Ser Glu Tyr Asp Ala Arg Val Val Ser Arg Phe Ala Glu 360
 350 355 360
 GGA GAC CCA GTA AGC ACC CGC ATC GTG GGC TCC CAC TGC GAA TCC GGC 3318
 Gly Asp Pro Val Ser Thr Arg Ile Val Gly Ser His Cys Glu Ser Gly 375
 365 370 375
 10 GAT ATC CTG ATC AAC GAT GAA ATC TAC CCA TCT GAC ATC ACC AGC GGC 3366
 Asp Ile Leu Ile Asn Asp Glu Ile Tyr Pro Ser Asp Ile Thr Ser Gly 390
 380 385 390
 GAC TTC CTT GCA CTC GCA GCC ACC GGC GCA TAC TGC TAC GCC ATG AGC 3414
 Asp Phe Leu Ala Leu Ala Ala Thr Gly Ala Tyr Cys Tyr Ala Met Ser 405
 395 400 405
 15 TCC CGC TAC AAC GCC TTC ACA CGG CCC GCC GTC GTG TCC GTC CGC GCT 3462
 Ser Arg Tyr Asn Ala Phe Thr Arg Pro Ala Val Ser Val Arg Ala 425
 410 415 420 425
 GGC AGC TCC CGC CTC ATG CTG CGC CGC GAA ACG CTC GAC GAC ATC CTC 3510
 Gly Ser Ser Arg Leu Met Leu Arg Arg Glu Thr Leu Asp Asp Ile Leu 440
 430 435 440
 20 TCA CTA GAG GCA TAACGCTTTT CGACGCTGA CCCC GCCCTT CACCTTCGCC 3562
 Ser Leu Glu Ala 445
 GTGGAGGGCG GTTTTGG 3579
 25 (2) INFORMATION FOR SEQ ID NO:11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 550 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 Met Thr Pro Ala Asp Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu
 1 5 10 15
 Val Leu Thr Ser Arg Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val
 20 25 30
 35 Val Val Glu Arg Pro Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn
 35 40 45
 Ile Ala Leu Gln Val Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu
 50 55 60
 Ala Thr Trp Leu Ala Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser
 65 70 75 80
 40 Ala Glu Ile Ala Gly Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala
 85 90 95
 Ala Gln Gly Glu Ile Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe
 100 105 110
 Gly Asn Ser Asp His Leu Ser His Leu Asp Val Asn Leu Glu Phe Val
 115 120 125
 45 Ser Ala Asn Pro Thr Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala
 130 135 140
 Ala Val Gly Asp Ser Leu Gly Arg Val Leu Glu Ala Ser Gly Ala Lys
 145 150 155 160
 50 Val Thr Arg Glu Tyr Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg
 165 170 175
 Phe Ala Leu Ser Leu Leu Ala Ala Ala Lys Gly Glu Pro Thr Pro Glu
 180 185 190

Asp Gly Tyr Gly Gly Glu Tyr Ile Lys Glu Ile Ala Glu Ala Ile Val
 195 200 205
 Glu Lys His Pro Glu Ala Leu Ala Leu Glu Pro Ala Ala Thr Gln Glu
 210 215 220
 Leu Phe Arg Ala Glu Gly Val Glu Met Met Phe Glu His Ile Lys Ser
 225 230 235 240
 Ser Leu His Glu Phe Gly Thr Asp Phe Asp Val Tyr Tyr His Glu Asn
 245 250 255
 Ser Leu Phe Glu Ser Gly Ala Val Asp Lys Ala Val Gln Val Leu Lys
 260 265 270
 Asp Asn Gly Asn Leu Tyr Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser
 275 280 285
 Thr Glu Phe Gly Asp Asp Lys Asp Arg Val Val Ile Lys Ser Asp Gly
 290 295 300
 Asp Ala Ala Tyr Ile Ala Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe
 305 310 315 320
 Ser Arg Gly His Asn Leu Asn Ile Tyr Met Leu Gly Ala Asp His His
 325 330 335
 Gly Tyr Ile Ala Arg Leu Lys Ala Ala Ala Ala Leu Gly Tyr Lys
 340 345 350
 Pro Glu Gly Val Glu Val Leu Ile Gly Gln Met Val Asn Leu Leu Arg
 355 360 365
 Asp Gly Lys Ala Val Arg Met Ser Lys Arg Ala Gly Thr Val Val Thr
 370 375 380
 Leu Asp Asp Leu Val Glu Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser
 385 390 395 400
 Leu Ile Arg Ser Ser Val Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu
 405 410 415
 Trp Glu Ser Gln Ser Ser Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly
 420 425 430
 His Ala Arg Leu Cys Ser Ile Ala Arg Lys Ala Glu Thr Leu Gly Val
 435 440 445
 Thr Glu Glu Gly Ala Asp Leu Ser Leu Leu Thr His Asp Arg Glu Gly
 450 455 460
 Asp Leu Ile Arg Thr Leu Gly Glu Phe Pro Ala Val Val Lys Ala Ala
 465 470 475 480
 Ala Asp Leu Arg Glu Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu
 485 490 495
 Ala Gly Thr Phe His Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys
 500 505 510
 Val Asp Glu Asp Thr Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala
 515 520 525
 Ala Ala Thr Arg Gln Thr Leu Ala Asn Ala Leu His Leu Val Gly Val
 530 535 540
 Ser Ala Pro Glu Lys Met
 545 550

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
 1 5 10 15
 Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
 20 25 30

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5 Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
 35 40 45
 Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
 50 55 60
 Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
 65 70 75 80
 Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
 85 90 95
 10 Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
 100 105 110
 Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
 115 120 125
 Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
 130 135 140
 15 Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
 145 150 155 160
 Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
 165 170 175
 Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
 180 185 190
 20 Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
 195 200 205
 Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
 210 215 220
 Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
 225 230 235 240
 25 Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
 245 250 255
 Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala
 260 265 270
 Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu
 275 280 285
 30 Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile
 290 295 300
 Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp
 305 310 315 320
 Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly
 325 330 335
 35 Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp
 340 345 350
 Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg
 355 360 365
 40 Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu
 370 375 380
 Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala
 385 390 395 400
 Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr
 405 410 415
 45 Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu
 420 425 430
 Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
 435 440 445

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"
5 (iv) ANTI-SENSE: no
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
TCGTCGGTCA GCCTGACGTC GAC

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(2) INFORMATION FOR SEQ ID NO:14:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
15 (A) DESCRIPTION: /desc = "synthetic DNA"
(iv) ANTI-SENSE: yes
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
TCTTGGTGTCGAAAGTGCACACC

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(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3533 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
25 (ii) MOLECULE TYPE: genomic DNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Brevibacterium lactofermentum
(B) STRAIN: ATCC 13869
(ix) FEATURE:
(A) NAME/KEY: CDS
30 (B) LOCATION: 321..3077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
GGTGGTTCTG TTAAGGCAGA AACCGTCGCT GAGATCGTCG GTCAGCCTGA CGTCGACGGC 60
GGACTTGTCG GTGGCGCTTC CCTCGACGGT GAAGCATTCG CCAAGCTGGC TGCCAACGCT 120
GCGAGCGTTG CTTAAAGTAC AGAGCTTTAA AGCACAGCCT TAAAGCACAG CCTTAAAGCA 180
CAAGCACTGT AGAAGTGCGG TTTTGATGAG CCCATGAAAG CCATCGAAAT CAATCGCCCA 240
35 GCTAAACACC TGTGTTGCTG GGTGATTTT TATCTCATGC ACGCCAACAC CCTCAATGTG 300
AAAGAGTGTT TAAAGTAGTT ATG ACT GAT TTT TTA CGC GAT GAC ATC AGG 350
Met Thr Asp Phe Leu Arg Asp Asp Ile Arg
1 5 10
TTC CTC GGT CAA ATC CTC GGT GAG GTA ATT GCG GAA CAA GAA GGC CAG 398
40 Phe Leu Gly Gln Ile Leu Gly Glu Val Ile Ala Glu Gln Glu Gly Gln
15 20 25
GAG GTT TAT GAA CTG GTC GAA CAA GCG CGC CTG ACT TCT TTT GAT ATC 446
Glu Val Tyr Glu Leu Val Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile
30 35 40
GCC AAG GGC AAC GCC GAA ATG GAT AGC CTG GTT CAG GTT TTC GAC GGC 494
45 Ala Lys Gly Asn Ala Glu Met Asp Ser Leu Val Gln Val Phe Asp Gly
45 50 55
ATT ACT CCA GCC AAG GCA ACA CCG ATT GCT CGC GCA TTT TCC CAC TTC 542
Ile Thr Pro Ala Lys Ala Thr Pro Ile Ala Arg Ala Phe Ser His Phe
60 65 70
50 GCT CTG CTG GCT AAC CTG GCG GAA GAC CTC TAC GAT GAA GAG CTT CGT 590
Ala Leu Leu Ala Asn Leu Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg
75 80 85 90

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	GAA	CAG	GCT	CTC	GAT	GCA	GGC	GAC	ACC	CCT	CCG	GAC	AGC	ACT	CTT	GAT	638
	Glu	Gln	Ala	Leu	Asp	Ala	Gly	Asp	Thr	Pro	Pro	Asp	Ser	Thr	Leu	Asp	
				95						100					105		
5	GCC	ACC	TGG	CTG	AAA	CTC	AAT	GAG	GGC	AAT	GTT	GGC	GCA	GAA	GCT	GTG	686
	Ala	Thr	Trp	Leu	Lys	Leu	Asn	Glu	Gly	Asn	Val	Gly	Ala	Glu	Ala	Val	
				110					115					120			
	GCC	GAT	GTG	CTG	CGC	AAT	GCT	GAG	GTG	GCG	CCG	GTT	CTG	ACT	GCG	CAC	734
	Ala	Asp	Val	Leu	Arg	Asn	Ala	Glu	Val	Ala	Pro	Val	Leu	Thr	Ala	His	
				125					130					135			
10	CCA	ACT	GAG	ACT	CGC	CGC	CGC	ACT	GTT	TTT	GAT	GCG	CAA	AAG	TGG	ATC	782
	Pro	Thr	Glu	Thr	Arg	Arg	Arg	Thr	Val	Phe	Asp	Ala	Gln	Lys	Trp	Ile	
		140						145				150					
	ACC	ACC	CAC	ATG	CGT	GAA	CGC	CAC	GCT	TTG	CAG	TCT	GCG	GAG	CCT	ACC	830
	Thr	Thr	His	Met	Arg	Glu	Arg	His	Ala	Leu	Gln	Ser	Ala	Glu	Pro	Thr	
		155				160				165					170		
15	GCT	CGT	ACG	CAA	AGC	AAG	TTG	GAT	GAG	ATC	GAG	AAG	AAC	ATC	CGC	CGT	878
	Ala	Arg	Thr	Gln	Ser	Lys	Leu	Asp	Glu	Ile	Glu	Lys	Asn	Ile	Arg	Arg	
				175					180					185			
	CGC	ATC	ACC	ATT	TTG	TGG	CAG	ACC	GCG	TTG	ATT	CGT	GTG	GCC	CGC	CCA	926
	Arg	Ile	Thr	Ile	Leu	Trp	Gln	Thr	Ala	Leu	Ile	Arg	Val	Ala	Arg	Pro	
				190					195					200			
20	CGT	ATC	GAG	GAC	GAG	ATC	GAA	GTA	GGG	CTG	CGC	TAC	TAC	AAG	CTG	AGC	974
	Arg	Ile	Glu	Asp	Glu	Ile	Glu	Val	Gly	Leu	Arg	Tyr	Tyr	Lys	Leu	Ser	
			205					210				215					
	CTT	TTG	GAA	GAG	ATT	CCA	CGT	ATC	AAC	CGT	GAT	GTG	GCT	GTT	GAG	CTT	1022
	Leu	Leu	Glu	Glu	Ile	Pro	Arg	Ile	Asn	Arg	Asp	Val	Ala	Val	Glu	Leu	
		220					225					230					
25	CGT	GAG	CGT	TTC	GGC	GAG	GAT	GTT	CCT	TTG	AAG	CCC	GTG	GTC	AAG	CCA	1070
	Arg	Glu	Arg	Phe	Gly	Glu	Asp	Val	Pro	Leu	Lys	Pro	Val	Val	Lys	Pro	
		235			240					245					250		
	GGT	TCC	TGG	ATT	GGT	GGA	GAC	CAC	GAC	GGT	AAC	CCT	TAT	GTC	ACC	GCG	1118
	Gly	Ser	Trp	Ile	Gly	Gly	Asp	His	Asp	Gly	Asn	Pro	Tyr	Val	Thr	Ala	
				255					260					265			
	GAA	ACA	GTT	GAG	TAT	TCC	ACT	CAC	CGC	GCT	GCG	GAA	ACC	GTG	CTC	AAG	1166
	Glu	Thr	Val	Glu	Tyr	Ser	Thr	His	Arg	Ala	Ala	Glu	Thr	Val	Leu	Lys	
			270						275					280			
35	TAC	TAT	GCA	CGC	CAG	CTG	CAT	TCC	CTC	GAG	CAT	GAG	CTC	AGC	CTG	TCG	1214
	Tyr	Tyr	Ala	Arg	Gln	Leu	His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	
			285					290						295			
	GAC	CGC	ATG	AAT	AAG	GTC	ACC	CCG	CAG	CTG	CTT	GCG	CTG	GCA	GAT	GCC	1262
	Asp	Arg	Met	Asn	Lys	Val	Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	
			300				305					310					
40	GGG	CAC	AAC	GAC	GTG	CCA	AGC	CGC	GTG	GAT	GAG	CCT	TAT	CGA	CGC	GCC	1310
	Gly	His	Asn	Asp	Val	Pro	Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	
			315			320					325				330		
	GTC	CAT	GGC	GTT	CGC	GGA	CGT	ATC	CTC	GCG	ACG	ACG	GCC	GAG	CTG	ATC	1358
	Val	His	Gly	Val	Arg	Gly	Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	
				335					340					345			
45	GGC	GAG	GAC	GCC	GTT	GAG	GGC	GTG	TGG	TTC	AAG	GTC	TTT	ACT	CCA	TAC	1406
	Gly	Glu	Asp	Ala	Val	Glu	Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	
			350					355						360			
	GCA	TCT	CCG	GAA	GAA	TTC	TTA	AAC	GAT	GCG	TTG	ACC	ATT	GAT	CAT	TCT	1454
	Ala	Ser	Pro	Glu	Glu	Phe	Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	
			365					370					375				
50	CTG	CGT	GAA	TCC	AAT	GAC	GTT	CTC	ATT	GCC	GAT	GAT	CGT	TTG	TCT	GTG	1502
	Leu	Arg	Glu	Ser	Asn	Asp	Val	Leu	Ile	Ala	Asp	Asp	Arg	Leu	Ser	Val	
			380				385					390					

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	CTG ATT TCT GCC ATC GAG AGC TTT GGA TTC AAC CTT TAC GCA CTG GAT	1550
	Leu Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp	
	395 400 405 410	
5	CTG CGC CAA AAC TCC GAA AGC TAC GAG GAC GTC CTC ACC GAG CTT TTC	1598
	Leu Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe	
	415 420 425	
	GAA CGC GCC CAA GTC ACC GCA AAC TAC CGC GAG CTG TCT GAA GCA GAG	1646
	Glu Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu	
	430 435 440	
10	AAG CTT GAG GTG CTG CTG AAG GAA CTG CGC AGC CCT CGT CCG CTG ATC	1694
	Lys Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile	
	445 450 455	
	CCG CAC GGT TCA GAT GAA TAC AGC GAG GTC ACC GAC CGC GAG CTC GGC	1742
	Pro His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly	
	460 465 470	
15	ATC TTC CGC ACC GCG TCG GAG GCT GTT AAG AAA TTC GGG CCA CGG ATG	1790
	Ile Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met	
	475 480 485 490	
	GTG CCT CAC TGC ATC ATC TCC ATG GCA TCA TCG GTC ACC GAT GTG CTC	1838
	Val Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu	
	495 500 505	
20	GAG CCG ATG GTA TTG CTC AAG GAA TTC GGC CTC ATT GCA GCG AAC GGC	1886
	Glu Pro Met Val Leu Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly	
	510 515 520	
	GAC AAC CCA CGC GGC ACC GTC GAT GTC ATC CCA CTG TTC GAA ACC ATC	1934
	Asp Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile	
25	525 530 535	
	GAA GAT CTC CAG GCC GGC GCC GGA ATC CTC GAC GAA CTG TGG AAA ATT	1982
	Glu Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile	
	540 545 550	
	GAT CTT TAC CGC AAC TAC CTC CTG CAG CGC GAC AAC GTC CAG GAA GTC	2030
	Asp Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val	
30	555 560 565 570	
	ATG CTC GGT TAC TCC GAT TCC AAC AAG GAT GGC GGA TAT TTC TCC GCA	2078
	Met Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala	
	575 580 585	
	AAC TGG GCG CTT TAC GAC GCG GAA CTG CAG CTC GTC GAA CTA TGC CGA	2126
	Asn Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg	
35	590 595 600	
	TCA GCC GGG GTC AAG CTT CGC CTG TTC CAC GGC CGT GGT GGC ACC GTC	2174
	Ser Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val	
	605 610 615	
40	GGC CGC GGT GGC GGA CCT TCC TAC GAC GCG ATT CTT GCC CAG CCC AGG	2222
	Gly Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg	
	620 625 630	
	GGG GCT GTC CAA GGT TCC GTG CGC ATC ACC GAG CAG GGC GAG ATC ATC	2270
	Gly Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile	
	635 640 645 650	
45	TCC GCT AAG TAC GGC AAC CCC GAA ACC GCG CGC CGA AAC CTC GAA GCT	2318
	Ser Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala	
	655 660 665	
	CTG GTC TCA GCA ACG CTT GAG GCA TCG CTT CTC GAC GTC TCC GAA CTC	2366
	Leu Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu	
	670 675 680	
50	ACC GAT CAC CAA CGC GCG TAC GAC ATC ATG AGT GAG ATC TCT GAG CTC	2414
	Thr Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu	
	685 690 695	

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	AGC TTG AAG AAG TAC GCC TCC TTG GTG CAC GAG GAT CAA GGC TTC ATC	2462
	Ser Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile	
	700 705 710	
5	GAT TAC TTC ACC CAG TCC ACG CCG CTG CAG GAG ATT GGA TCC CTC AAC	2510
	Asp Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn	
	715 720 725 730	
	ATC GGA TCC AGG CCT TCC TCA CGC AAG CAG ACC TCC TCG GTG GAA GAT	2558
	Ile Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp	
	735 740 745	
10	TTG CGA GCA ATC CCG TGG GTG CTC AGT TGG TCC CAG TCT CGT GTC ATG	2606
	Leu Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met	
	750 755 760	
	CTG CCG GGC TGG TTT GGT GTC GGC ACC GCA CTT GAG CAA TGG ATT GGC	2654
	Leu Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly	
	765 770 775	
15	GAA GGG GAG CAG GCC ACC CAG CGC ATT GCC GAG CTA CAA ACA CTC AAC	2702
	Glu Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn	
	780 785 790	
	GAG TCC TGG CCA TTT TTC ACC TCA GTG TTG GAT AAC ATG GCT CAG GTG	2750
	Glu Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val	
	795 800 805 810	
20	ATG TCC AAG GCA GAG CTG CGT TTG GCA AAG CTC TAC GCA GAC CTG ATC	2798
	Met Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile	
	815 820 825	
	CCA GAT AGG GAA GTA GCT GAG CGC GTT TAT GCC GTC ATC CGC GAG GAA	2846
	Pro Asp Arg Glu Val Ala Glu Arg Val Tyr Ala Val Ile Arg Glu Glu	
	830 835 840	
25	TAC TTC CTG ACC AAG AAG ATG TTC TGC GTA ATC ACC GGT TCT GAT GAT	2894
	Tyr Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp	
	845 850 855	
	CTG CTT GAT GAC AAC CCG CTT CTC GCA CGA TCC GTC CAG CGC CGA TAC	2942
	Leu Leu Asp Asp Asn Pro Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr	
	860 865 870	
30	CCC TAC CTG CTT CCA CTC AAC GTG ATC CAG GTA GAG ATG ATG CGA CGC	2990
	Pro Tyr Leu Leu Pro Leu Asn Val Ile Gln Val Glu Met Met Arg Arg	
	875 880 885 890	
	TAC CGA AAA GGC GAC CAA AGC GAG CAA GTA TCC CGC AAC ATC CAG CTG	3038
	Tyr Arg Lys Gly Asp Gln Ser Glu Gln Val Ser Arg Asn Ile Gln Leu	
	895 900 905	
35	ACC ATG AAC GGT CTT TCC ACT GCA CTG CGC AAC TCT GGC TAGTCCTGCT	3087
	Thr Met Asn Gly Leu Ser Thr Ala Leu Arg Asn Ser Gly	
	910 915	
	GGGTAGGTAG TACTCGTGTA TACTGTCTAA AGTTATTCGA AATCAGGTGG GAATAAGGTT	3147
40	CACCTGGGTT CTCAAACGGC AAAGGAACAT TTTCCACATG GCATTGACGC TTCAAATCAT	3207
	CCTCGTCGTC GCCAGCCTGC TCATGACGGT TTTTCGTCTTG CTGCACAAGG GCAAAGGCGG	3267
	CGGACTCTCC AGCCTCTTCG GTGGCGGTGT GCAGTCCAAT CTTTCGGGCT CCACTGTTGT	3327
	TGAAAAGAAC CTGGATCGCG TCACCATTTT GGTGCGCGTT ATCTGGATTG TGTGCATTGT	3387
	CGCACTCAAC CTCATCCAGA CTTATTCATA AGACACGAGC TTAAAAAGAG CGGTTCCCTT	3447
	TTCATAGGGG AGCCGCTTTT TTGGGTTTTG TCGACCTGTT GTCTCCCCAC TGTTCTCGG	3507
45	TGTGCACTTT CGACACCAAG ATTTTCG	3533

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 919 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu
1 5 10 15
Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val
20 25 30
5 Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu
35 40 45
Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala
50 55 60
Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu
65 70 75 80
10 Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala
85 90 95
Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu
100 105 110
15 Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn
115 120 125
Ala Glu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg
130 135 140
Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr Thr His Met Arg Glu
145 150 155 160
20 Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala Arg Thr Gln Ser Lys
165 170 175
Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp
180 185 190
Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Ile
195 200 205
25 Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Glu Glu Ile Pro
210 215 220
Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg Glu Arg Phe Gly Glu
225 230 235 240
Asp Val Pro Leu Lys Pro Val Val Lys Pro Gly Ser Trp Ile Gly Gly
245 250 255
30 Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu Thr Val Glu Tyr Ser
260 265 270
Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Ala Arg Gln Leu
275 280 285
His Ser Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Lys Val
290 295 300
35 Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly His Asn Asp Val Pro
305 310 315 320
Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val His Gly Val Arg Gly
325 330 335
Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly Glu Asp Ala Val Glu
340 345 350
40 Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala Ser Pro Glu Glu Phe
355 360 365
Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu Arg Glu Ser Asn Asp
370 375 380
Val Leu Ile Ala Asp Arg Leu Ser Val Leu Ile Ser Ala Ile Glu
385 390 395 400
45 Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu Arg Gln Asn Ser Glu
405 410 415
Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr
420 425 430
Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys Leu Glu Val Leu Leu
435 440 445
50 Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro His Gly Ser Asp Glu
450 455 460

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Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile Phe Arg Thr Ala Ser
 465 470 475 480
 Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile
 485 490 495
 5 Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu
 500 505 510
 Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr
 515 520 525
 10 Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu Asp Leu Gln Ala Gly
 530 535 540
 Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr
 545 550 555 560
 Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp
 565 570 575
 15 Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp
 580 585 590
 Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu
 595 600 605
 Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Pro
 610 615 620
 20 Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser
 625 630 635 640
 Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn
 645 650 655
 Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu
 660 665 670
 25 Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala
 675 680 685
 Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala
 690 695 700
 Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser
 705 710 715 720
 30 Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser
 725 730 735
 Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp
 740 745 750
 Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly
 755 760 765
 35 Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr
 770 775 780
 Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe
 785 790 795 800
 Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu
 805 810 815
 40 Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val Ala
 820 825 830
 Glu Arg Val Tyr Ala Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys
 835 840 845
 Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro
 850 855 860
 45 Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu
 865 870 875 880
 Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln
 885 890 895
 50 Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser
 900 905 910
 Thr Ala Leu Arg Asn Ser Gly
 915

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CGCGAGGTAC CACCTGTCAC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CAATCCAGGT ACCGGCAACC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGATCCCCAA TCGATACCTG GAA

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CGGTCATCG CCAAGTTTTT CTT

23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GTCGACGGAT CGCAAATGGC AAC

23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGATCCTTGA GCACCTTGCG CAG

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CATCTAAGTA TGCATCTCGG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(iv) ANTI-SENSE: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TGCCCCCTCGA GCTAAATTAG

20

Claims

1. A recombinant DNA autonomously replicable in cells of coryneform bacteria, comprising a DNA sequence coding for an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and a DNA sequence coding for a diaminopimelate decarboxylase.
2. The recombinant DNA according to claim 1, wherein said aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized is an aspartokinase originating from coryneform bacteria, and wherein said aspartokinase is a mutant aspartokinase in which an amino acid residue corresponding to a 279th alanine residue as counted from its N-terminal in the amino acid sequence shown in SEQ ID NO: 5 is changed into an amino acid residue other than alanine and other than acidic amino acid in its α -subunit, and an amino acid residue corresponding to a 30th alanine residue as counted from its N-terminal in the amino acid sequence shown in SEQ ID NO: 7 is changed into an amino acid residue other than alanine and other than acidic amino acid in its β -subunit.
3. The recombinant DNA according to claim 1, wherein said DNA sequence coding for the diaminopimelate decarboxylase codes for an amino acid sequence shown in SEQ ID NO: 12, or an amino acid sequence substantially the same as the amino acid sequence shown in SEQ ID NO: 12.

4. The recombinant DNA according to claim 1, further comprising a DNA sequence coding for a phosphoenolpyruvate carboxylase.
5. A coryneform bacterium harboring an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and comprising an enhanced DNA sequence coding for a diaminopimelate decarboxylase.
6. The coryneform bacterium according to claim 5, transformed by introduction of the recombinant DNA as defined in claim 1.
7. The coryneform bacterium according to claim 5, further comprising an enhanced DNA sequence coding for a phosphoenolpyruvate carboxylase.
8. The coryneform bacterium according to claim 7, transformed by introduction of the recombinant DNA as defined in claim 4.
9. A method for producing L-lysine comprising the steps of cultivating said coryneform bacterium as defined in claim 5 in an appropriate medium to allow L-lysine to be produced and accumulated in a culture of the bacterium, and collecting L-lysine from the culture.

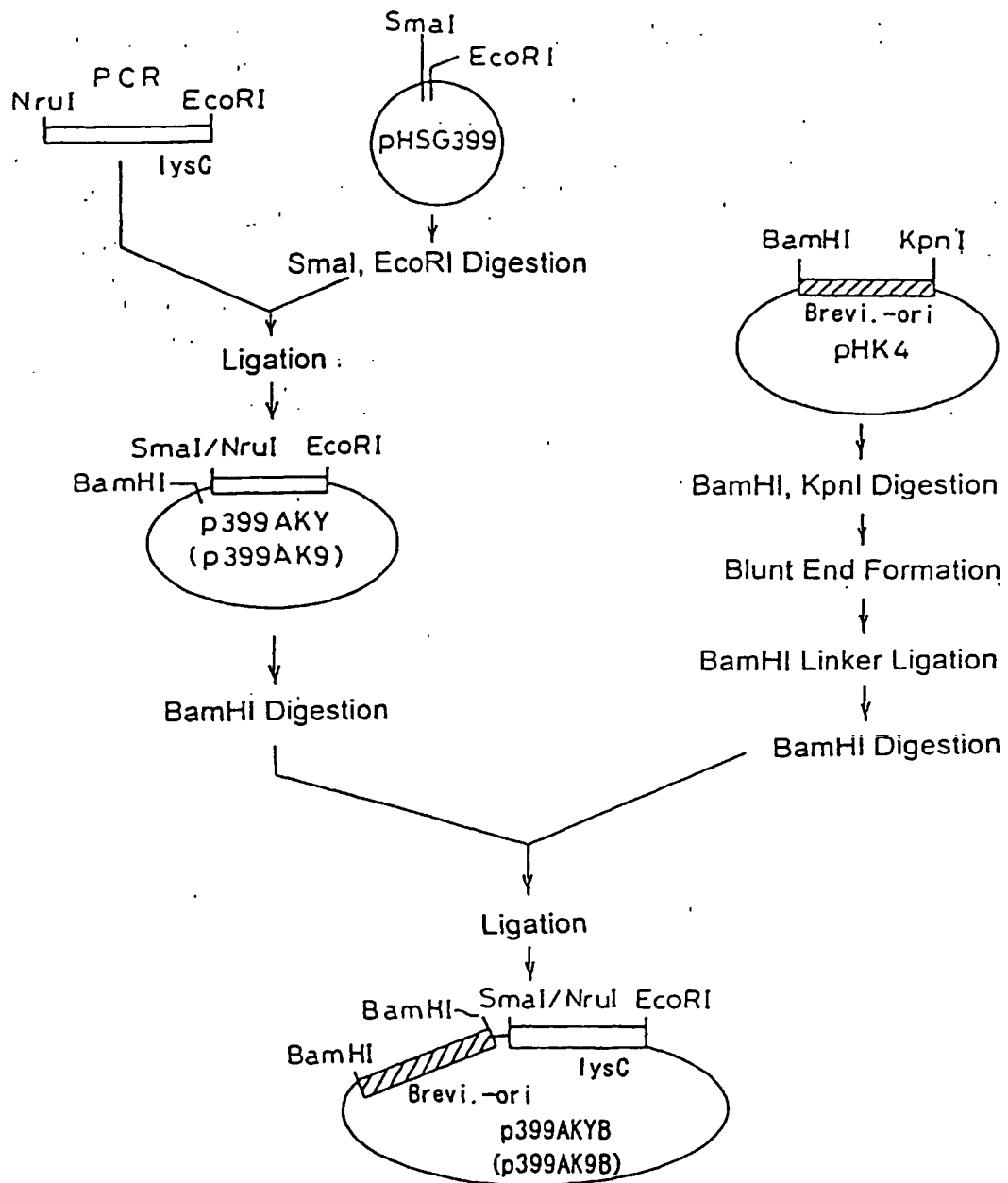


FIG. 1

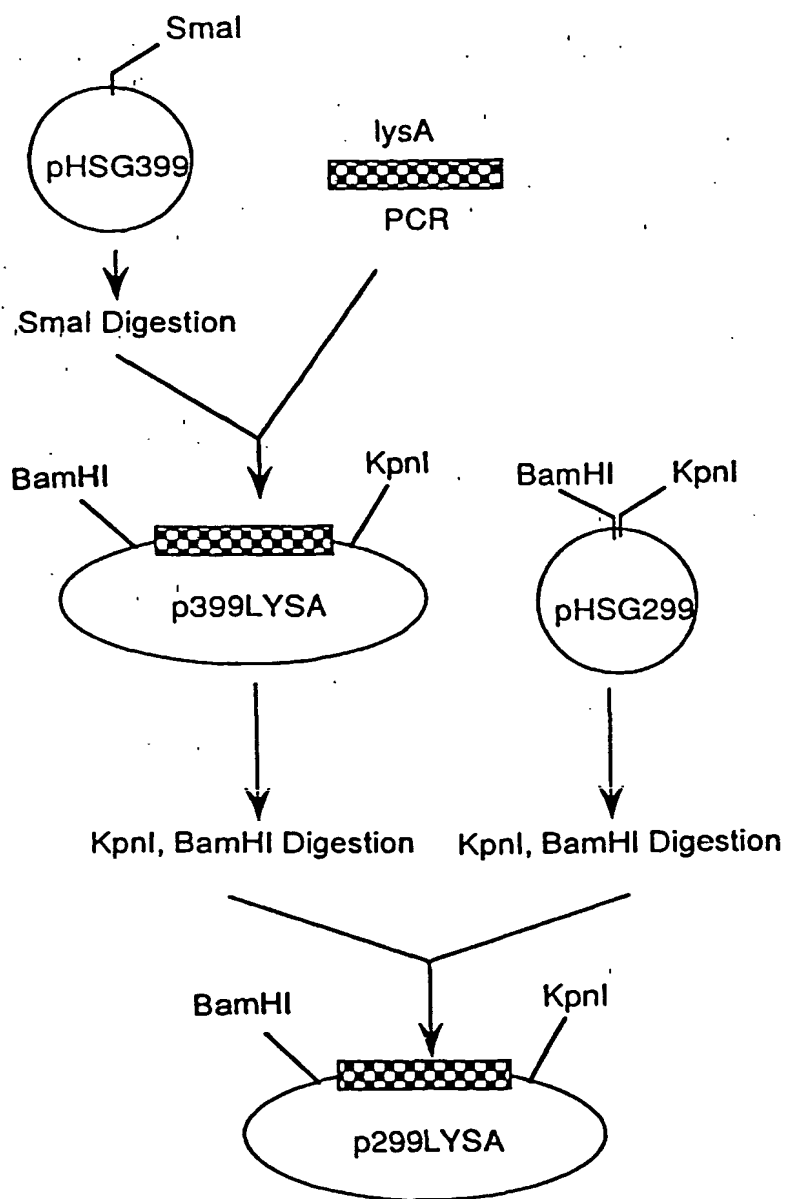


FIG. 2

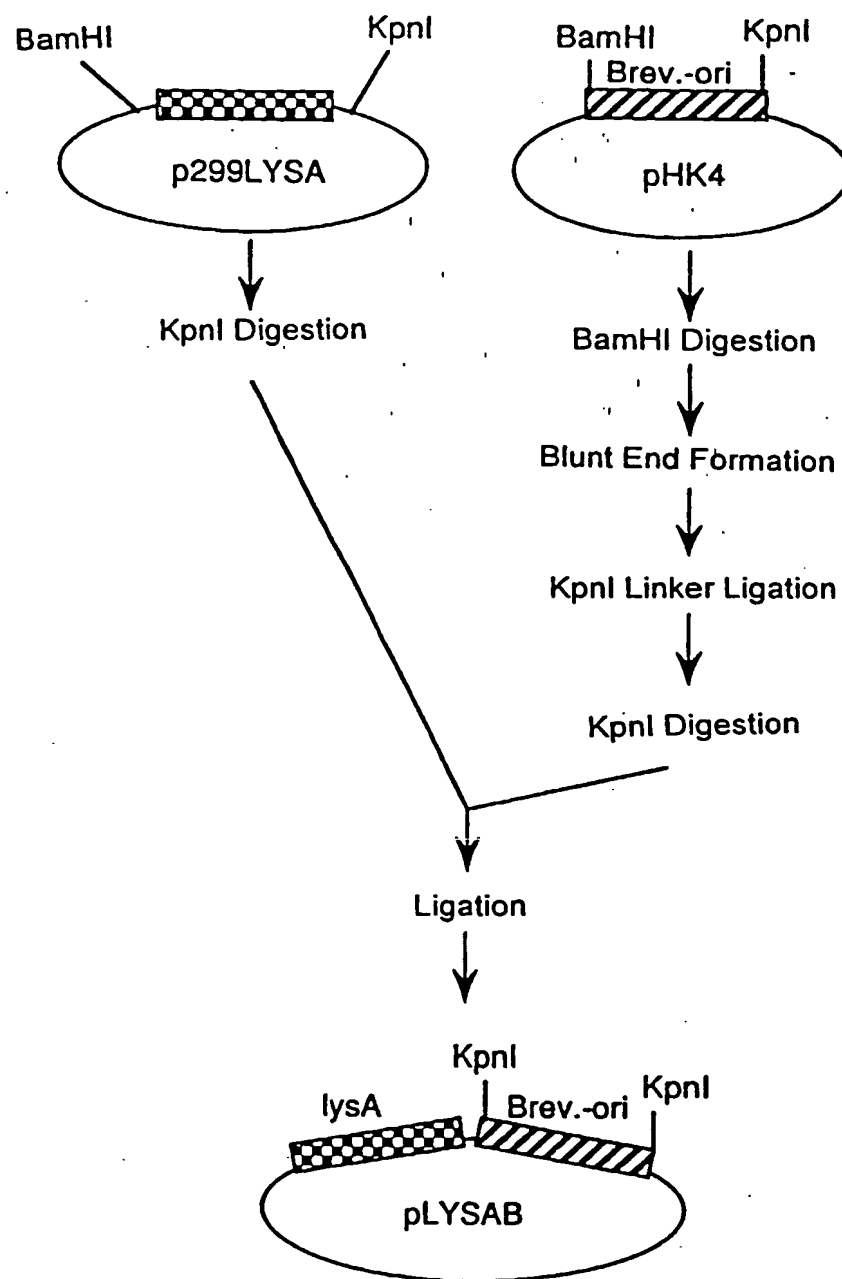


FIG. 3

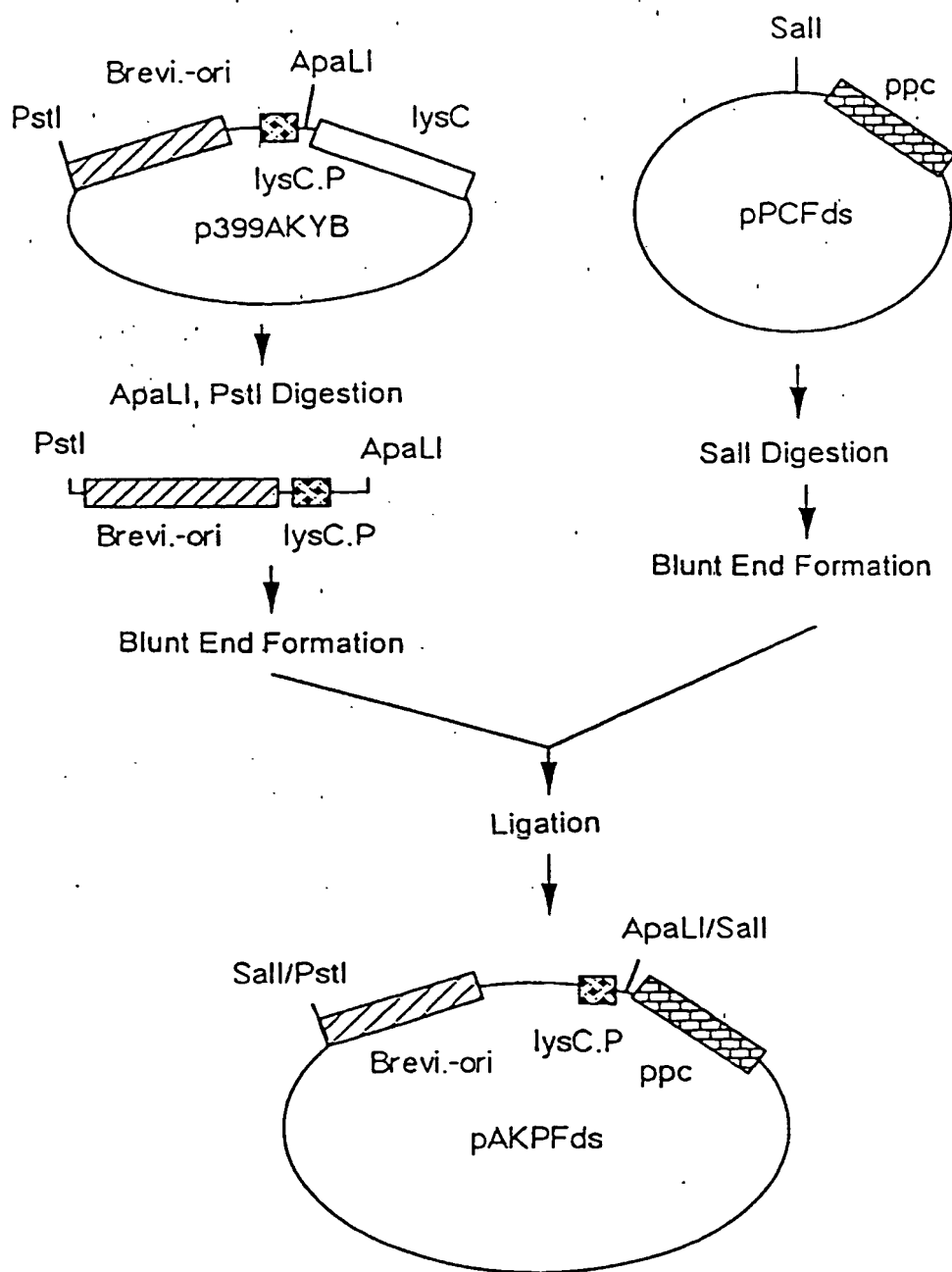


FIG. 4

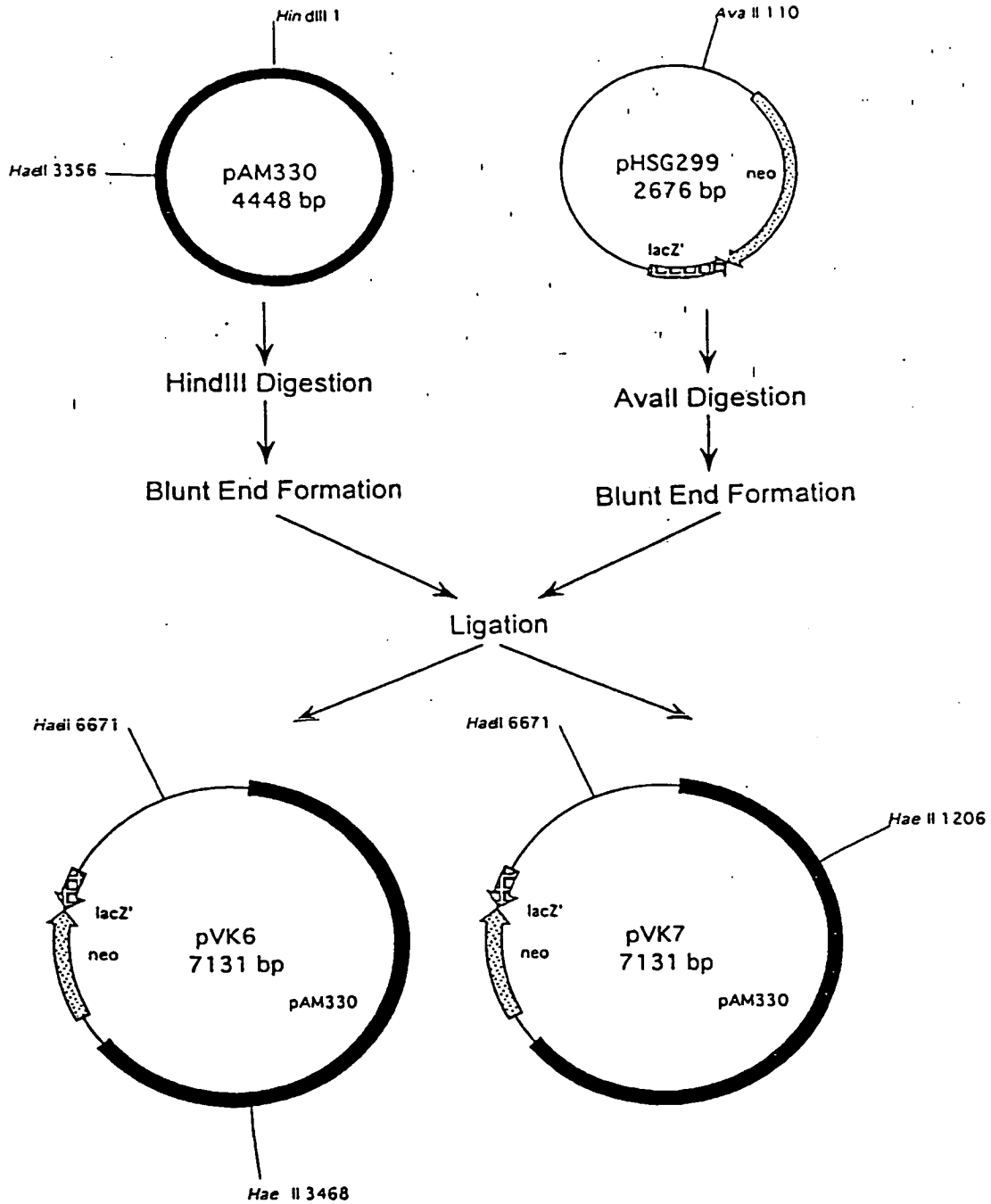


FIG. 5

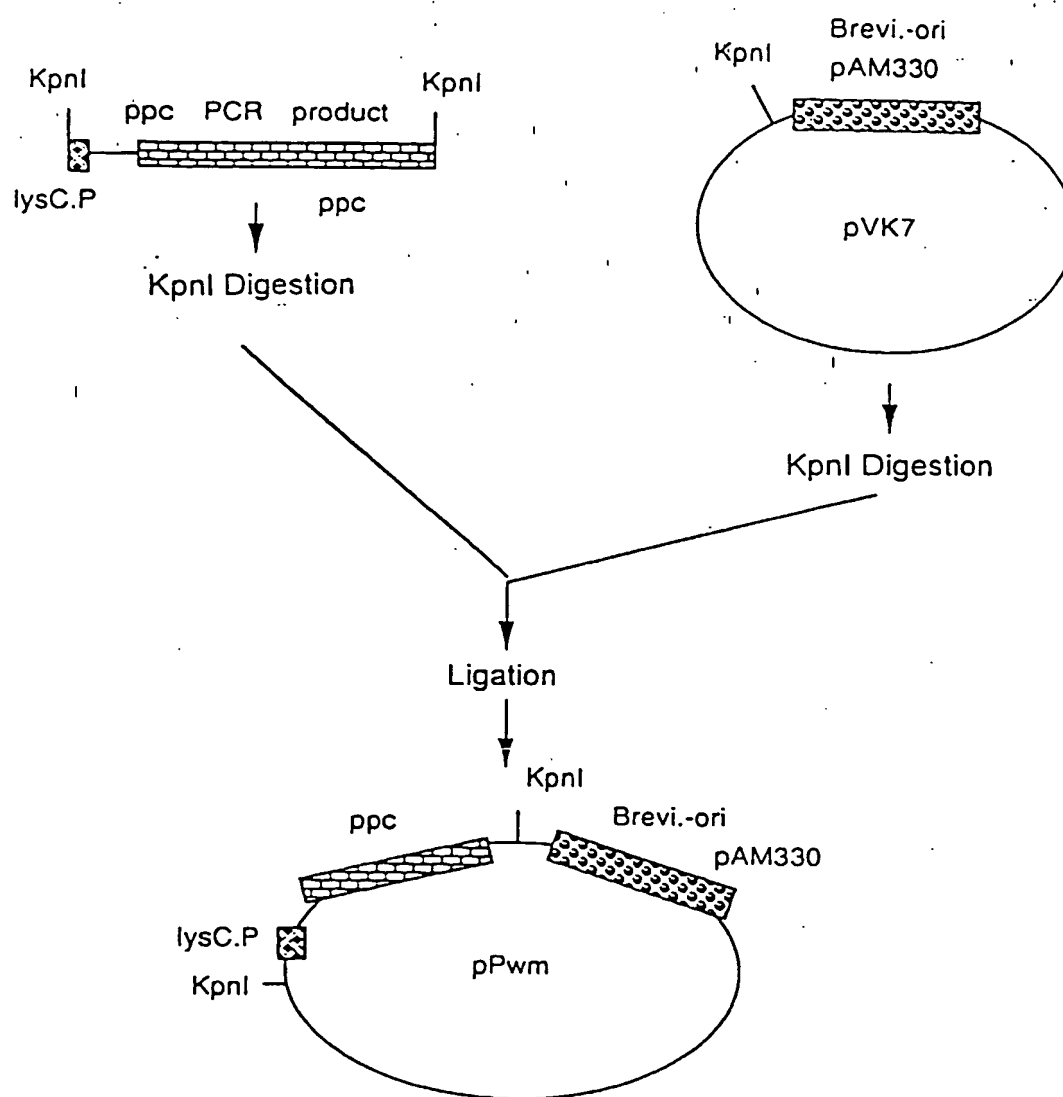


FIG. 6

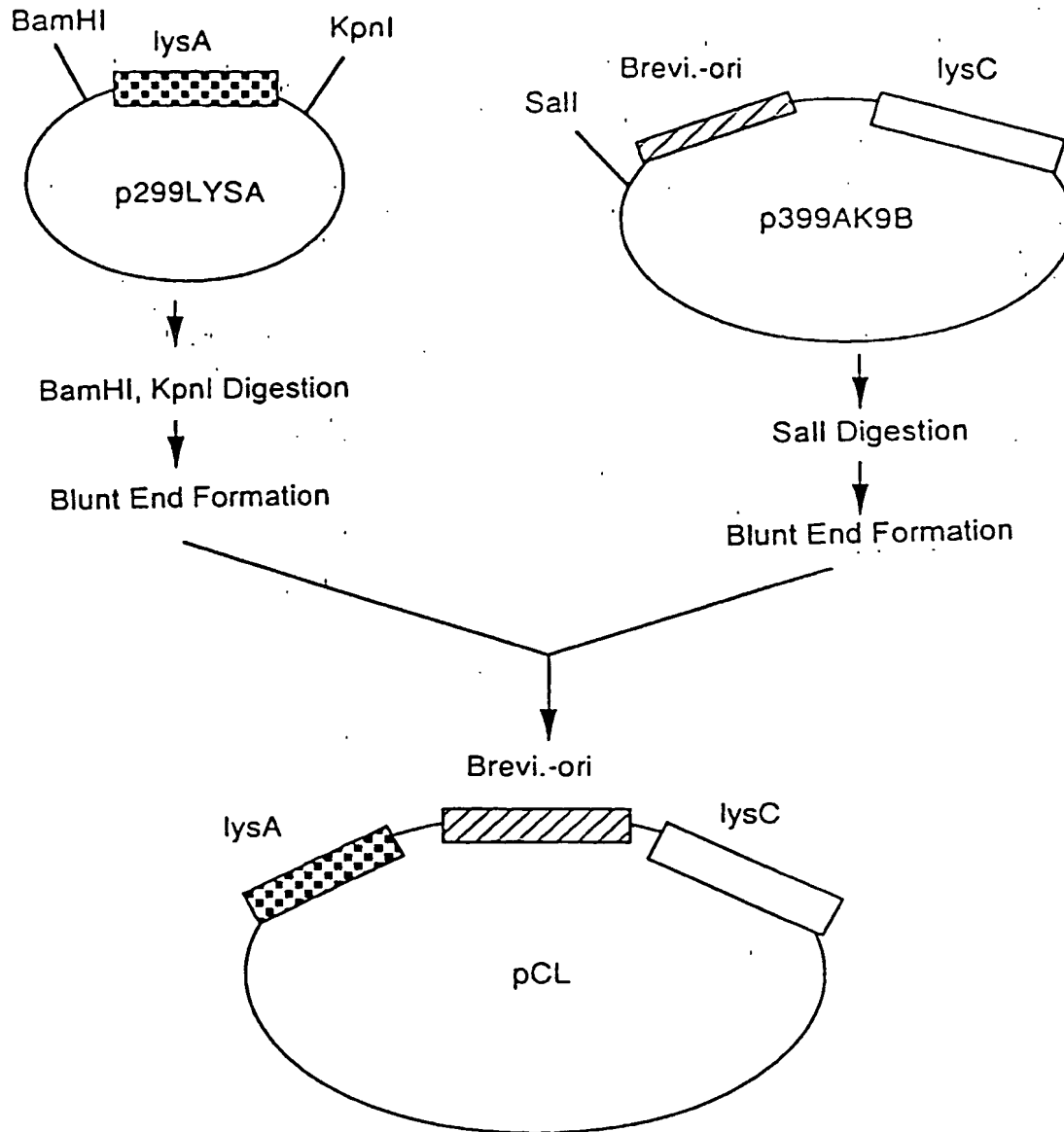


FIG. 7

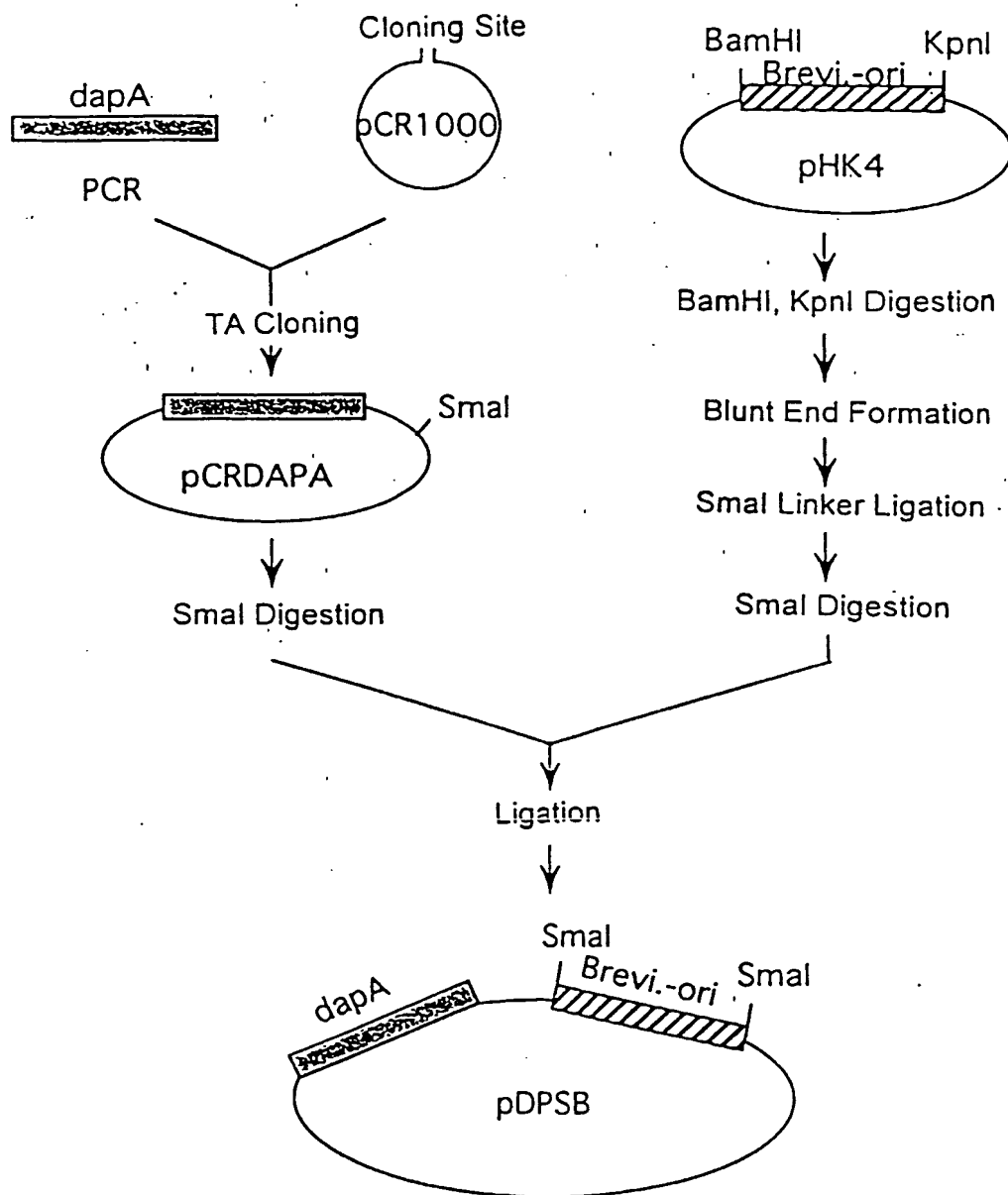


FIG. 8

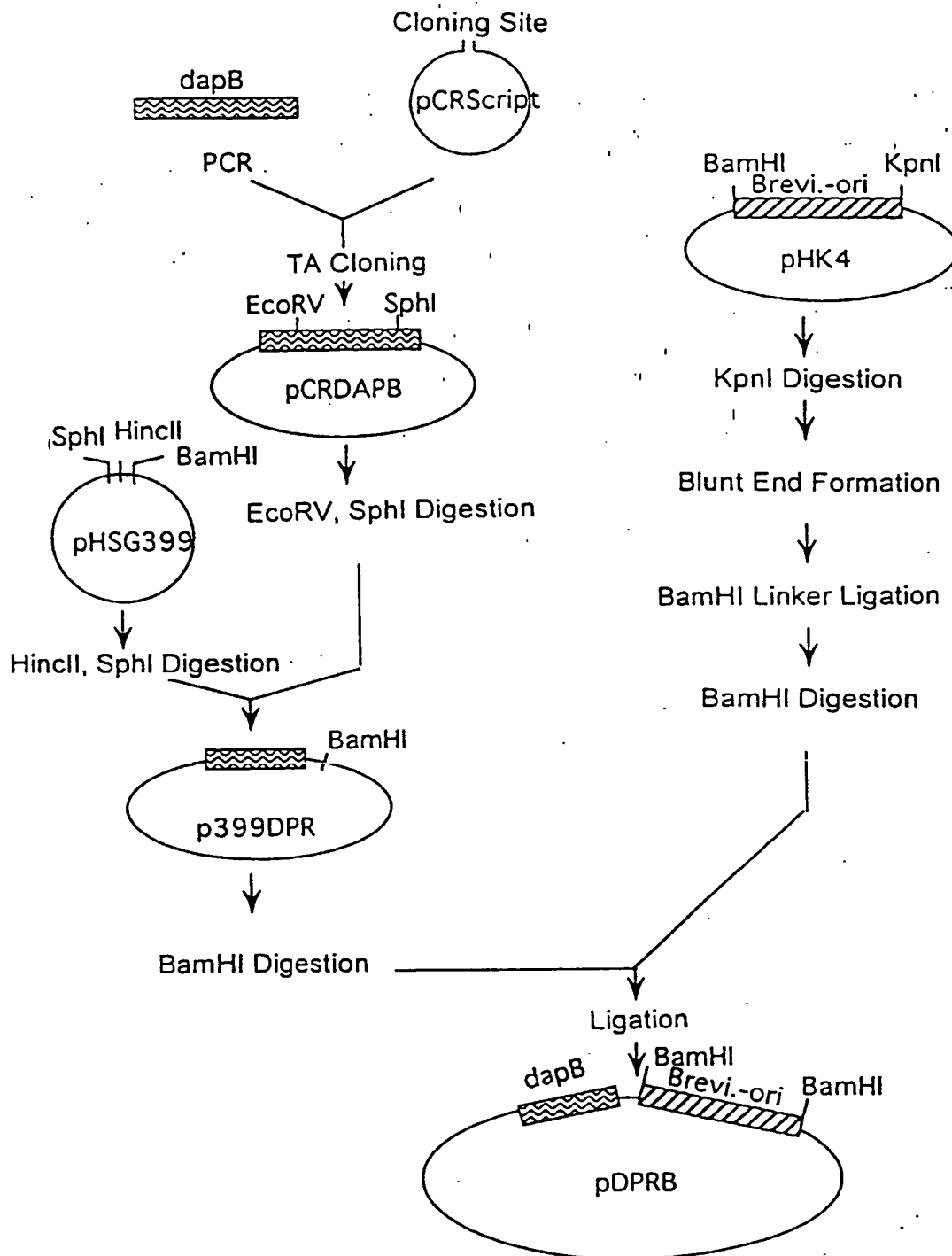


FIG. 9

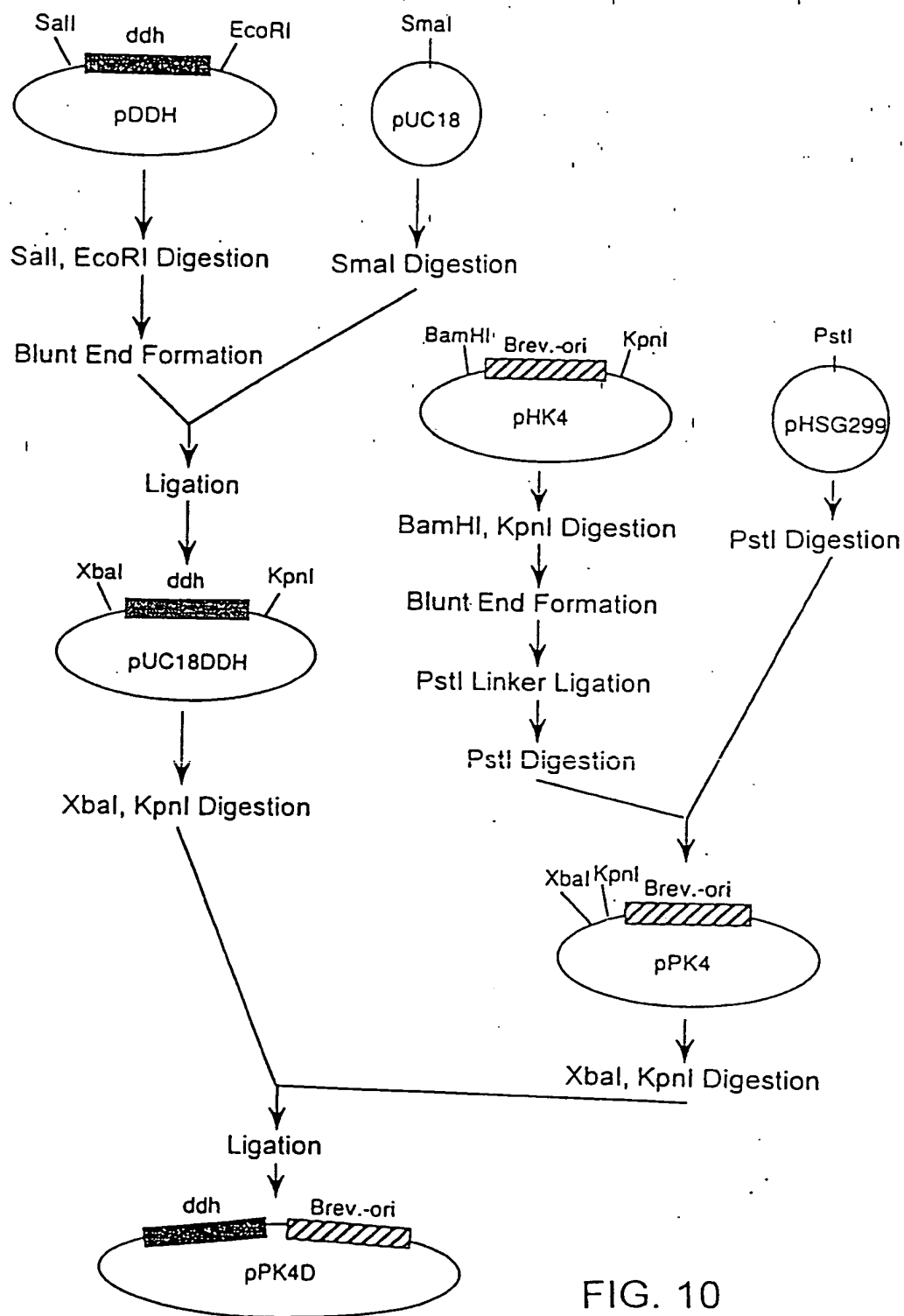


FIG. 10

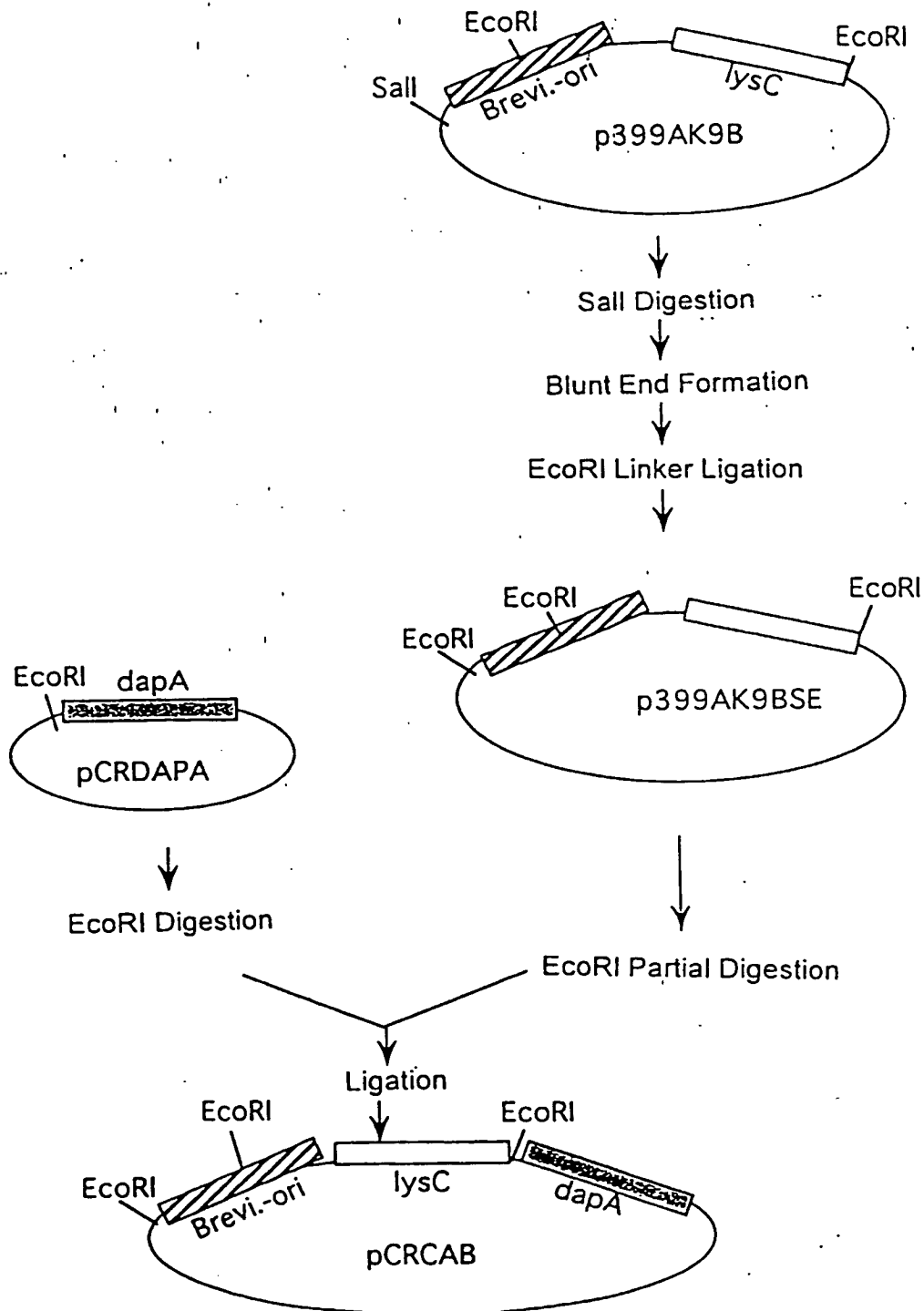


FIG. 11

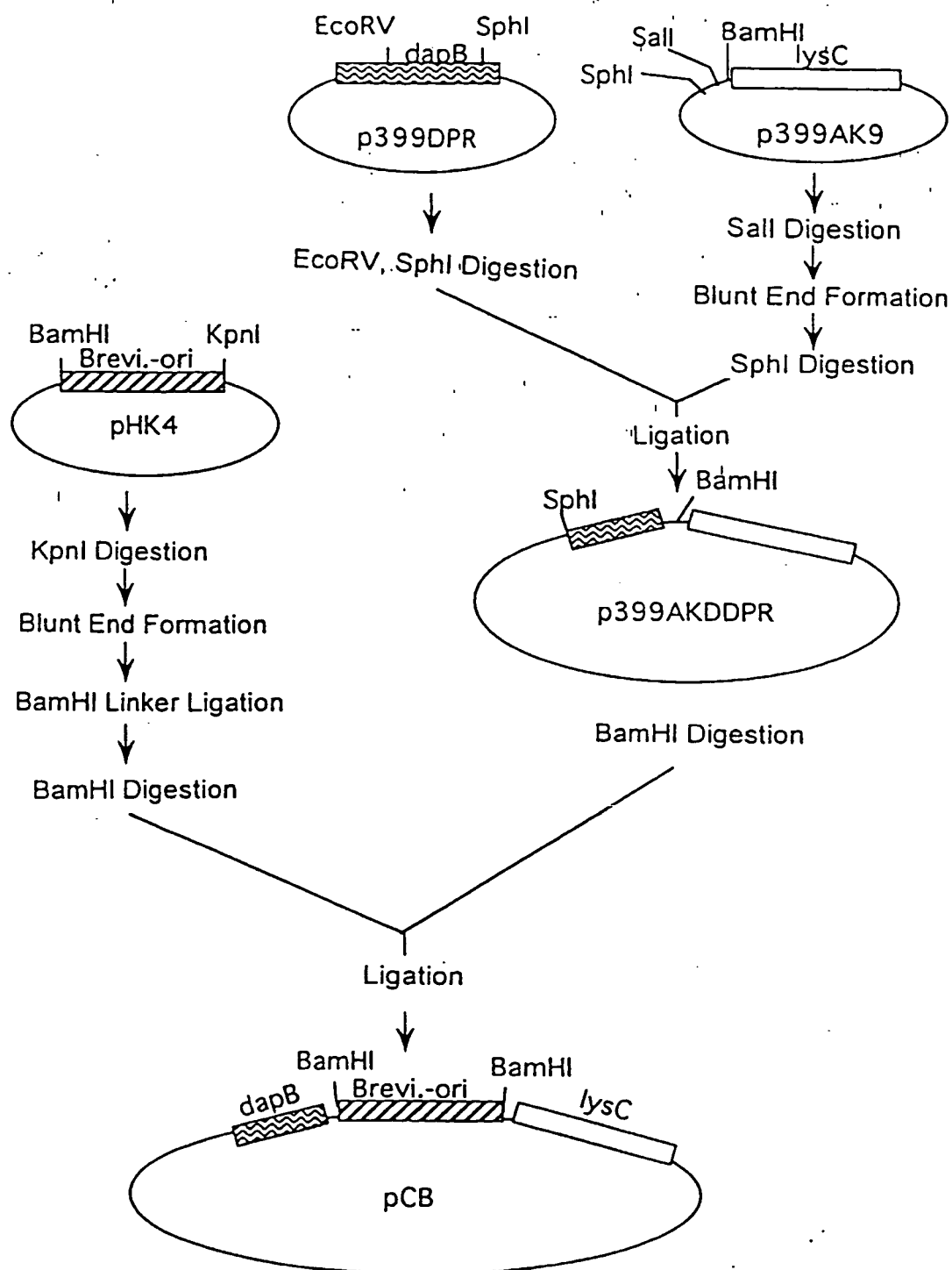


FIG. 12

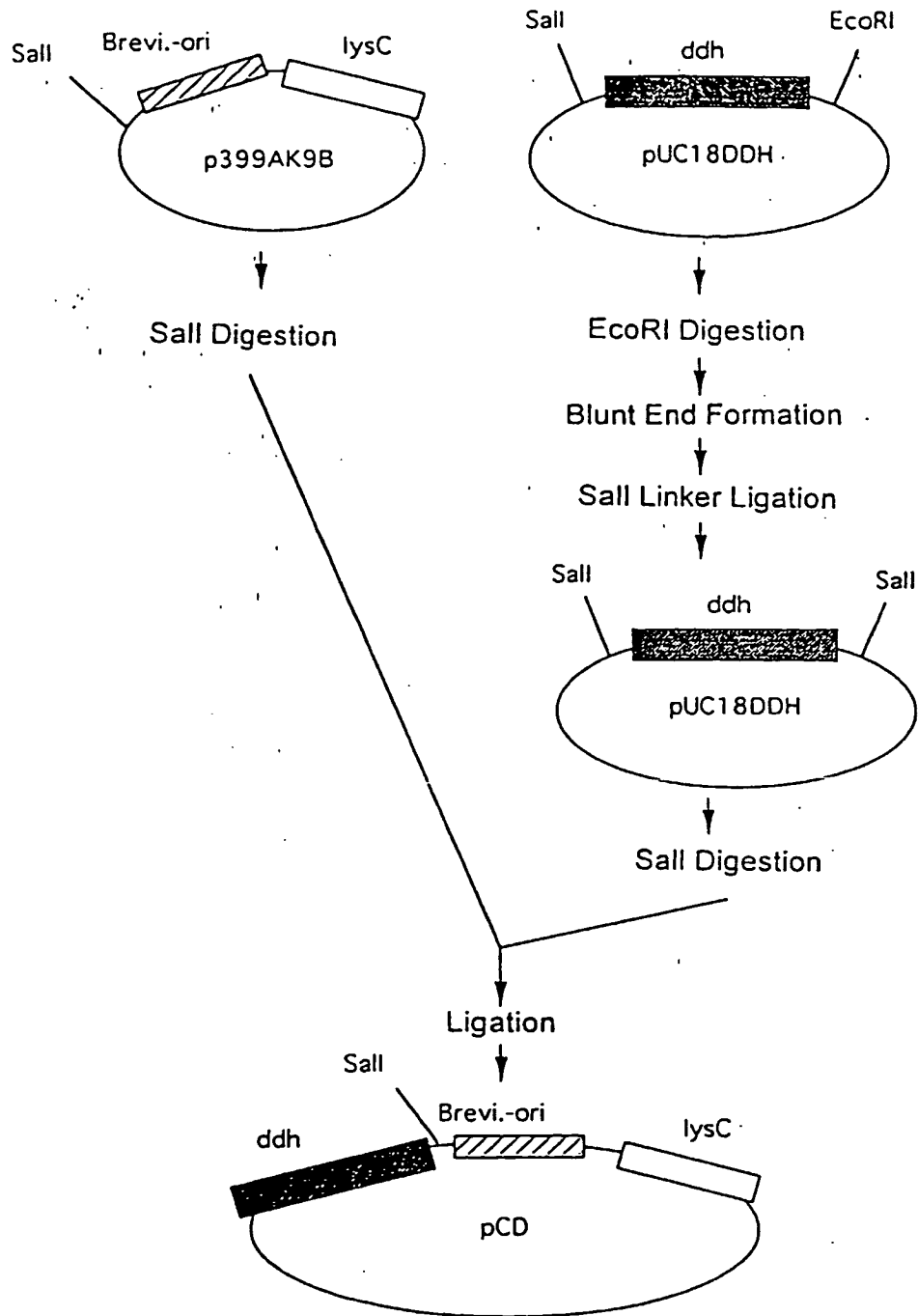


FIG. 13

(19)



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(11)

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(12)

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C12N 1/21
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(54) **Method for producing L-lysine**

(57) A recombinant DNA autonomously replicable in cells of coryneform bacteria, comprising a DNA sequence coding for an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensitized, and a DNA sequence coding for a diaminopimelate decarboxylase; a coryneform bacterium harboring an aspartokinase in which feedback inhibition by L-lysine and L-threonine is substantially desensi-

tized, and comprising an enhanced DNA sequence coding for a diaminopimelate decarboxylase; and a method for producing L-lysine comprising the steps of cultivating the coryneform bacterium in an appropriate medium to allow L-lysine to be produced and accumulated in a culture of the bacterium, and collecting L-lysine from the culture.

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EUROPEAN SEARCH REPORT

Application Number
EP 97 12 1444

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			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C12P
The present search report has been drawn up for all claims			
Place of search MUNICH		Date of completion of the search 31 July 2002	Examiner Weijland, A
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